Refine Search

Search Results -

Term	Documents
HEAT	3294346
HEATS	122347
SHOCK	419667
SHOCKS	72211
PROTEINS	246473
PROTEIN	383106
(35 AND ((HEAT ADJ SHOCK) ADJ PROTEINS)).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	29
(L35 AND HEAT SHOCK PROTEINS).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	29

Database:
US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L36

Refine Search

Recall Text | Clear | Interrupt

Search History

DATE: Wednesday, April 06, 2005 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L36	L35 and heat shock proteins	29	L36
L35	L34 and @py<2003	256	L35
L34	2-D gel	627	L34

L33	US 6331388 B1	2	L33
L32	L31 and protein same degradation same prevention	35	L32
L31	heat shock proteins and protease	2727	L31
L30	heat shock protein same prevent same protein same degradation	6	L30
L29	heat skock proteins same (2-D gel elctrophoresis) same prevent same degradation same protein	0	L29
L28	L27 and prevent protein degrdation	0	L28
L27	L26 and protease	493	L27
L26	L25 and composition	764	L26
L25	L24 and @py<2003	847	L25
L24	L23 and method	2184	L24
L23	L22 and prevent	2184	L23
L22	heat shock proteins and degradation	2742	L22
L21	2-D gel same heat shock proteins	8	L21
L20	2-D gel same heat shock proteins same use same degradation	0	L20
L19	L15 and protein degradation	5	L19
L18	L15 and HSP26	0	L18
L17	L15 and IbpB	0	L17
L16	L15 and IbpA	0	L16
L15	L14 and electrophoresis	64	L15
L14	L13 and L11	68	L14
L13	heat shock proteins	6432	L13
L12	L11 and heat shock proteins|HSP	5831	L12
L11	2-D gel	627	L11
L10	2-D gel same heat shock proteins	8	L10
L9	US 5320951	3	L9
L8	US 5175096	2	L8
DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L7	decorin same clot formation same kit	2	L7
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L6	decorin same clot formation	4	L6
L5	decorin same antithrombotic	3	L5
L4	decorin same anticoagulating	3	L4
L3	L2 and N-terminal	36	L3
L2	decorin same glycosaminoglycan	96	L2
L1	antithrombotic same decorin same proteoglycan same glycosaminoglycan	0	L1

END OF SEARCH HISTORY

Refine Search

Search Results -

Term	Documents
HSP	3955
HSPS	2141
(16 AND HSP).PGPB,USPT.	3
(L16 AND HSP).PGPB,USPT.	3

Database:
US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L17

Refine Search

Recall Text Clear Interrupt

Search History

DATE: Wednesday, April 13, 2005 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L17	L16 and HSP	3	L17
L16	L15 and @py<2003	59	L16
L15	proteomes same gel electrophoresis	400	L15
L14	L13 and heat shock proteins	3	L14
L13	L12 and @py<2003	37	L13
L12	L11 and 2-D gel	162	L12
L11	proteomes	1371	L11
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L10	L9 and @py<2003	72	L10
L9	L7 and gel electrophoresis	118	L9
L8	L7 and protein degradation	9	L8

L7	small heat shock proteins	201	L7
L6	L5 and @py<2003	16	L6
L5	L4 and degradation	57	L5
L4	L3 and composition	158	L4
L3	L2 and py<2003	201	L3
L2	small heat shock proteins	201	L2
L1	small heat shock proteins composition	0	L1

END OF SEARCH HISTORY

```
Connecting via Winsock to STN



Welcome to STN International!  Enter x:x

LOGINID:SSSPTA1647

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2          "Ask CAS" for self-help around the clock
 NEWS  3  FEB 25  CA/CAPLUS - Russian Agency for Patents and Trademarks
                  (ROSPATENT) added to list of core patent offices covered
 NEWS  4  FEB 28  PATDPAFULL - New display fields provide for legal status
                  data from INPADOC
 NEWS  5  FEB 28  BABS - Current-awareness alerts (SDIs) available
 NEWS  6  FEB 28  MEDLINE/LMEDLINE reloaded
 NEWS  7  MAR 02  GBFULL: New full-text patent database on STN
 NEWS  8  MAR 03  REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS  9  MAR 03  MEDLINE file segment of TOXCENTER reloaded
 NEWS  10 MAR 22  KOREAPAT now updated monthly; patent information enhanced
 NEWS  11 MAR 22  Original IDE display format returns to REGISTRY/ZREGISTRY
 NEWS  12 MAR 22  PATDPASPC - New patent database available
 NEWS  13 MAR 22  REGISTRY/ZREGISTRY enhanced with experimental property tags
 NEWS  14 APR 04  EPFULL enhanced with additional patent information and new
                  fields
 NEWS  15 APR 04  EMBASE - Database reloaded and enhanced

 NEWS EXPRESS  JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
  agreement.  Please note that this agreement limits use to scientific
  research.  Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005

=> file caplus
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                 0.21       0.21

FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005
```

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is
held by the publishers listed in the PUBLISHER (PB) field (available
for records published or updated in Chemical Abstracts after December
26, 1996), unless otherwise indicated in the original publications.
The CA Lexicon is the copyrighted intellectual property of the
American Chemical Society and is provided to assist you in searching
databases on STN. Any dissemination, distribution, copying, or storing
of this information, without the prior written consent of CAS, is
strictly prohibited.

FILE COVERS 1907 - 6 Apr 2005 VOL 142 ISS 15
FILE LAST UPDATED: 5 Apr 2005 (20050405/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s @-D gel
       2189555 D
        458143 GEL
         92335 GELS
        494175 GEL
                  (GEL OR GELS)
L1        1052 @-D GEL
                  (D(W)GEL)

=> s heat skock proteins
       1211478 HEAT
         53338 HEATS
       1225064 HEAT
                  (HEAT OR HEATS)
             2 SKOCK
       1200566 PROTEINS
             4 PROTEINSES
       1200570 PROTEINS
                  (PROTEINS OR PROTEINSES)
L2           0 HEAT SKOCK PROTEINS
                  (HEAT(W)SKOCK(W)PROTEINS)

=> s heat skock protein
       1211478 HEAT
         53338 HEATS
       1225064 HEAT
                  (HEAT OR HEATS)
             2 SKOCK
       1729771 PROTEIN
       1200566 PROTEINS
       2008504 PROTEIN
                  (PROTEIN OR PROTEINS)
L3           0 HEAT SKOCK PROTEIN
                  (HEAT(W)SKOCK(W)PROTEIN)

=> s chapaerone
             0 CHAPAERONE
L4           0 CHAPAERONE

=> s HSP
         15201 HSP
          2046 HSPS
```

```
L5       15629 HSP
                (HSP OR HSPS)

=> d his

     (FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

     FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005
L1          1052 S @-D GEL
L2             0 S HEAT SKOCK PROTEINS
L3             0 S HEAT SKOCK PROTEIN
L4             0 S CHAPAERONE
L5         15629 S HSP

=> s L1 and L5
L6            42 L1 AND L5

=> s L6 and protein
       1729771 PROTEIN
       1200566 PROTEINS
       2008504 PROTEIN
                (PROTEIN OR PROTEINS)
L7            42 L6 AND PROTEIN

=> s L7 and prevention and denaturation
         278897 PREVENTION
            122 PREVENTIONS
         278952 PREVENTION
                (PREVENTION OR PREVENTIONS)
          34803 DENATURATION
            158 DENATURATIONS
          34846 DENATURATION
                (DENATURATION OR DENATURATIONS)
L8             0 L7 AND PREVENTION AND DENATURATION

=> s L7 and prevention
         278897 PREVENTION
            122 PREVENTIONS
         278952 PREVENTION
                (PREVENTION OR PREVENTIONS)
L9             0 L7 AND PREVENTION

=> d his

     (FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

     FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005
L1          1052 S @-D GEL
L2             0 S HEAT SKOCK PROTEINS
L3             0 S HEAT SKOCK PROTEIN
L4             0 S CHAPAERONE
L5         15629 S HSP
L6            42 S L1 AND L5
L7            42 S L6 AND PROTEIN
L8             0 S L7 AND PREVENTION AND DENATURATION
L9             0 S L7 AND PREVENTION

=> d L7 1-10 ibib,abs

L7   ANSWER 1 OF 42  CAPLUS  COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER:         2005:133528  CAPLUS
DOCUMENT NUMBER:          142:238591
TITLE:                    Proteomic profiling of human stem cells derived from
                          umbilical cord blood
```

AUTHOR(S): Zenzmaier, Christoph; Gesslbauer, Bernd; Grobuschek, Nina; Jandrositz, Anita; Preisegger, Karl-Heinz; Kungl, Andreas J.
CORPORATE SOURCE: Lifecord Inc., Graz, A-8010, Austria
SOURCE: Biochemical and Biophysical Research Communications (2005), 328(4), 968-972
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB CD34+ prepns. from five different umbilical cord samples were compared with respect to their proteome profile using 2-**D gel** electrophoresis. Fifty-two **protein** spots were found to match in all prepns. referring to the high heterogeneity of such samples indicating a not fully developed (or instable) proteome of stem cells. All matching spots were subjected to in-gel digestion and nano-LC-MS/MS sequence anal., from which 22 **proteins** were unambiguously identified.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1067027 CAPLUS
TITLE: Differential signatures of **protein** expression in marmoset liver and thymus induced by single-dose TCDD treatment
AUTHOR(S): Oberemm, Axel; Meckert, Christine; Brandenburger, Linda; Herzig, Andrea; Lindner, Yvonne; Kalenberg, Kareen; Krause, Eberhard; Ittrich, Carina; Kopp-Schneider, Annette; Stahlmann, Ralf; Richter-Reichhelm, Hans-Bernhard; Gundert-Remy, Ursula
CORPORATE SOURCE: Federal Institute for Risk Assessment, Berlin, 14195, Germany
SOURCE: Toxicology (2005), 206(1), 33-48
CODEN: TXCYAC; ISSN: 0300-483X
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is an ubiquitously distributed environmental pollutant. Health effects have been studied intensively, but low-dose effects are quite complex and not yet fully understood. In many studies, the immune system was identified as the most sensitive target. Here, we demonstrate changes of **protein** expression in liver and thymus of male marmosets (Callithrix jacchus) which were subjected to a single dose of a s.c. injection of 100 ng/kg body weight TCDD. Histopathol. examination revealed myocardial fibrosis, but there were no significant findings in pathol. and histopathol. of liver and thymus. In order to detect more subtle treatment-related changes, we performed a comparative proteomic investigation of liver and thymus using a 2-**D gel** electrophoresis based proteomics approach. Fluorescence labeling and automated image anal. was used to enhance sensitivity and reproducibility. In both organs, distinct changes of **protein** expression were detected which were more pronounced in thymus, where the pattern of deregulated **proteins** could be clearly related to immune responses. In the thymus of treated animals, several toxicol. relevant factors were increased, including chaperones, glycerol-3-phosphate dehydrogenase, and adseverin. Among others, vimentin, Ca-dependent protease and **protein** disulfide isomerase were downregulated. In the liver, transferrins, lamin A and HSP70 were upregulated, whereas thymidine phosphorylase (synonyms: endothelial cell growth factor, PD-ECGF, gliostatin) was significantly reduced. Comparative anal. of deregulated **proteins** in both organs revealed a pattern of related functions, which fits well into the existing knowledge of the toxic processes and mechanisms underlying TCDD-mediated toxicity.

REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1029346 CAPLUS
DOCUMENT NUMBER: 142:110541
TITLE: Proteomic analysis of the response of Arabidopsis chloroplast **proteins** to high light stress
AUTHOR(S): Phee, Bong-Kwan; Cho, Jin-Hwan; Park, Sebyul; Jung, Jin Hee; Lee, Youn-Hyung; Jeon, Jong-Seong; Bhoo, Seong Hee; Hahn, Tae-Ryong
CORPORATE SOURCE: Graduate School of Biotechnology and Plant Metabolism Research Center, Kyung Hee University, Suwon, S. Korea
SOURCE: Proteomics (2004), 4(11), 3560-3568
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 μmol photons·m-2·s-1) conditions and then subjected to high light (1000 μmol photons·m-2·s-1) stress. Chloroplasts were then isolated from these plants and both soluble and insol. **proteins** were extracted and subjected to two-dimensional (2-**D**) **gel** electrophoresis. The resolved **proteins** were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database anal. 64 **Protein** spots, which were identified as candidate factors that responded to high light stress, were then selected for anal. and 52 of these were successfully identified using MALDI-TOF-MS anal. 35 Of the 52 identified **proteins** were found to decrease their expression levels during high light stress and a further 14 of the candidate **proteins** had upregulated expression levels under these conditions. Most of the **proteins** that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated **proteins** were identified as previously well-known high light stress-related **proteins**, such as heat shock **proteins** (**HSPs**), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel **proteins** that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.
REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1013025 CAPLUS
DOCUMENT NUMBER: 142:20704
TITLE: Localization of the chaperone **proteins** GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa
AUTHOR(S): Boilard, M.; Reyes-Moreno, C.; Lachance, C.; Massicotte, L.; Bailey, J. L.; Sirard, M.-A.; Leclerc, P.
CORPORATE SOURCE: Departement des Sciences Animales, Centre de Recherche en Biologie de la Reproduction, Universite Laval, Quebec, QC, G1K 7P4, Can.

SOURCE: Biology of Reproduction (2004), 71(6), 1879-1889
CODEN: BIREBV; ISSN: 0006-3363
PUBLISHER: Society for the Study of Reproduction
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no **protein** candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane exts., either an oviductal factor triggered intracellular events resulting in pos. effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a pos. action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with [35S]-methionine and, upon extensive washes, **proteins** were separated by two-dimensional (2-**D**) **gel** electrophoresis to identify the factors suspected to have beneficial effects on spermatozoa. The six major **proteins**, according to their signal intensity on the autoradiog. film, were extracted from a 2-**D gel** of oviduct epithelial cell **proteins** run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to heat shock **protein** 60 (HSP60) and one to the glucose-regulated **protein** 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these **proteins**. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:767842 CAPLUS
DOCUMENT NUMBER: 142:357
TITLE: Proteomic analysis of **proteins** altered by dibenzoylmethane in human prostatic cancer LNCaP cells
AUTHOR(S): Frazier, Monica C.; Jackson, Kimberly M.; Jankowska-Stephens, Ewa; Anderson, Mark G.; Harris, Wayne B.
CORPORATE SOURCE: CBR/RCMI and Cancer Center, Tuskegee University, Tuskegee, AL, USA
SOURCE: Proteomics (2004), 4(9), 2814-2821
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This paper explores the use of proteomics as a tool for identifying **protein** species whose expression has been altered by dibenzoylmethane (DBM) in LNCaP cells. Although DBM, a constituent of licorice, has been shown to induce cell cycle arrest and regulate androgen receptor (AR) expression, the mechanism by which these events occur is unknown. To develop a better understanding of the effect of DBM on cancer cells, the authors analyzed changes in **protein** expression induced by DBM in LNCaP cells using two-dimensional (2-**D**) **gel** electrophoresis. The proteomic approach used to study LNCaP cells has lead to the anal. and identification of a number of **protein** species that increase or decrease as a result of exposure to DBM. In

particular, twenty features were differentially expressed in this study based on the quantitation of two sep. 2-D-fluorescence difference gel electrophoresis analyses. Thirteen of these features were identified through mass spectrometric anal. The intensity of 10 out of the 13 spots identified increased 2- to 3-fold in response to 25 μM and 50 μM DBM and the remaining three spots decreased 2-fold in response to the same DBM treatment. This study investigates proteomic changes induced by treatment of cells with DBM to develop a model for the mechanism by which DBM induces cell cycle arrest and represses AR expression.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:637204 CAPLUS
DOCUMENT NUMBER: 141:256616
TITLE: Differential proteomic analysis of intestinal epithelium cell line before and after irradiation by gamma-ray
AUTHOR(S): Zhang, Bo; Su, Yongping; Ai, Guoping; Liu, Xiaohong; Wei, Yongjiang; Wang, Fengchao; Cheng, Tianmin
CORPORATE SOURCE: College of Preventive Medicine, Third Military Medical University, Chongqing, 400038, Peop. Rep. China
SOURCE: Di-San Junyi Daxue Xuebao (2003), 25(24), 2157-2160
CODEN: DYXUE8; ISSN: 1000-5404
PUBLISHER: Di-San Junyi Daxue Xuebao Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB Study the **proteins** associated with ionizing irradiation of intestinal epithelium cell line (IEC-6), and elucidate the mol. mechanism of reconstruction of intestinal epithelium damaged by ionizing irradiation **Protein** samples extracted from normal IEC-6 cells and IEC-6 cells irradiated by γ-ray at the dose of 25 Gy were separated by immobilized pH gradient two-dimensional (2-**D**) **gel** electrophoresis. After Coomasie blue staining, the 2-D electrophoretogram was analyzed using PDQuest software. The differential **proteins** were cut off from the Coomasie-blue stained gel and digested in gel with trypsin, and then identified by peptide mass fingerprinting based on matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) and database searching. Total RNA of IEC-6 cells was isolated and RT-PCR anal. was performed using primers of ERP29 and GAPDH. After Coomasie blue staining, the 2-DE image anal. by PDQuest software detected (608±39) spots in normal IEC-6 cell sample and (595 ± 31) spots in irradiated cells, of which 396 spots were matched. Sixteen differential spots were cut off from the Coomasie blue stained gel, and 11 spots were preliminarily identified. These **proteins** were associated with cell metabolism, cytoskeleton, and free radical elimination, etc.

Ionizing radiation induced mRNA of ERP29 in a time-dependent manner over a 48-h period. The results indicated that γ-ray irradiation can induce changes of the **protein** expression pattern of intestinal epithelium cell line. This helps to understand the mol. mechanisms of ionizing radiation on intestinal epithelium cells.

L7 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:579538 CAPLUS
DOCUMENT NUMBER: 141:222844
TITLE: Heat shock **protein** 70 (Hsp70) subtype expression in neuroendocrine tissue and identification of a neuroendocrine tumour-specific Hsp70 truncation
AUTHOR(S): Zierhut, B.; Mechtler, K.; Gartner, W.; Daneva, T.; Base, W.; Weissel, M.; Niederle, B.; Wagner, L.
CORPORATE SOURCE: Department of Medicine III, Division of Clinical Endocrinology and Metabolism, University of Vienna, Vienna, A-1090, Austria

SOURCE: Endocrine-Related Cancer (2004), 11(2), 377-389
CODEN: ERCAE9; ISSN: 1351-0088
PUBLISHER: Society for Endocrinology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In order to identify neuroendocrine tumor-specific **protein** expression, we generated monoclonal antibodies (mAbs) with a tumor-related reaction pattern using a human insulinoma as immunogen. One of the generated mAbs (mAb 1D4) exhibited striking immunoreactivity against various neuroendocrine tumors without staining pancreatic islets of Langerhans. Furthermore, mAb 1D4 immunostained a characteristic subtype of hypothalamic neurons. Using two-dimensional (2-**D**) **gel** electrophoresis, mAb 1D4 immunoblotting and mass spectrometry, heat shock **protein** 70 (Hsp70) isoforms were identified as the mAb 1D4-specific antigen. In hypothalamic tissue, the presence of two different Hsp70 isoforms (Hsp70-8 and Hsp70-1) was revealed by 2-**D** **gel** immunoblots and consecutive mass spectrometric peptide anal. In contrast, insulinoma and other neuroendocrine tumors displayed solely Hsp70-8 expression. Moreover, the tumor-specific presence of an addnl. mAb 1D4 immunoreactive **protein** of 40 kDa was observed in eight out of eight tested neuroendocrine tumors. For this variant, exclusively, peptides derived from the C terminus excluding the 299 amino-terminal residues were detected. In cultured tumor-derived fibroblasts, expression of the truncated Hsp70-8 subtype was not present. In conclusion, we have demonstrated a neuroendocrine tumor-specific expression pattern of Hsp70 isoforms and identified an as yet unknown N-terminally truncated Hsp70-8 variant.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:576084 CAPLUS
DOCUMENT NUMBER: 141:257757
TITLE: The proteome of chicken skeletal muscle: Changes in soluble **protein** expression during growth in a layer strain
AUTHOR(S): Doherty, Mary K.; McLean, Lynn; Hayter, Julia R.; Pratt, Julie M.; Robertson, Duncan H. L.; El-Shafei, Abdel; Gaskell, Simon J.; Beynon, Robert J.
CORPORATE SOURCE: Protein Function Group, Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, L69 7ZJ, UK
SOURCE: Proteomics (2004), 4(7), 2082-2093
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The whole animal, and the pectoralis muscle in particular, grows at a greatly enhanced rate in chickens selected for meat production (broilers) when compared to those selected for egg production (layers). As part of an ongoing study to analyze muscle **protein** dynamics under conditions of rapid growth, the authors have embarked upon a preliminary characterization of the proteome of layer chicken pectoralis muscle, at specified time-points from 1 to 27 days after hatching. Soluble exts. of muscle homogenates were separated by two-dimensional (2-**D**) **gel** electrophoresis and selected spots were analyzed by in-gel tryptic digestion and matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry. Of 90 spots, 51 gave mass spectra that matched to existing chicken **proteins** present in online databases, 12 matched equivalent **proteins** from non-avian species and 11 yielded good quality spectra but were unable to be matched against existing databases. For many of these **proteins**, growth over 27 days elicited dramatic changes in relative expression levels. Chicken skeletal muscle offers an excellent system for developmental proteomics.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:328454 CAPLUS
DOCUMENT NUMBER: 140:421867
TITLE: Nuclear matrix **protein** expressions in hepatocytes of normal and cirrhotic rat livers under normal and regenerating conditions
AUTHOR(S): Yun, Jing-Ping; Liew, Choong-Tsek; Chew, Eng Ching; Yin, Xiao-Yu; Lai, Paul Bo San; Fai, Yam Hin; Li, H. K. Richard; Jin, Mei-Lin; Ding, Ming-Xiao; Li, Ming-Tao; Lin, Han-Liang; Lau, Wan Yee
CORPORATE SOURCE: Department of Pathology, Cancer Center of Sun Yat-Sen University, Guangzhou, 510060, Peop. Rep. China
SOURCE: Journal of Cellular Biochemistry (2004), 91(6), 1269-1279
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We explored the feasibility of studying nuclear matrix **protein** (NMP) expressions of the hepatocytes in normal and cirrhotic rat livers with liver regeneration after partial hepatectomy. Sixteen Wistar healthy rats were studied with exptl. liver regeneration and/or liver cirrhosis. Two-dimensional (2-**D**) **gel** electrophoresis was used to generate these NMP compns. from these rat liver samples. Several antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and heat shock **protein** 70 were used for identification by Western blot. Totally, 41 strongly stained **protein** spots were characterized on the 2-**D gels**. Thirty-four **protein** spots were detected in all of these rat livers, of which, cytokeratin, vimentin, actin, HNF4α, and heat shock **protein** 70 were identified. B23 was detected in the regenerated livers. Three **protein** spots (s33, s34, and s35) were detectable only in NMP preparation extracted from the regenerating rat livers after hepatectomy. Another 3 **protein** spots (s36, s37, and s38) were detectable only in NMP preparation extracted from thioacetamide-induced cirrhotic rat livers. Under these conditions including exptl. liver regeneration and/or liver cirrhosis, Over thirty higher abundance NMPs of hepatocytes were consistently expressed and considered as common and basic NMPs. Some of the NMPs are specific for liver regeneration and may play a critical role in cell proliferation and cell cycle, and some are specific for liver cirrhosis.
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:161172 CAPLUS
DOCUMENT NUMBER: 140:284961
TITLE: F-actin capping (CapZ) and other contractile saphenous vein smooth muscle **proteins** are altered by hemodynamic stress: A proteomic approach
AUTHOR(S): McGregor, Emma; Kempster, Lee; Wait, Robin; Gosling, Martin; Dunn, Michael J.; Powell, Janet T.
CORPORATE SOURCE: Department of Vascular Surgery, Imperial College School of Medicine at Charing Cross Hospital, London, W6 8RP, UK
SOURCE: Molecular and Cellular Proteomics (2004), 3(2), 115-124
CODEN: MCPOBS; ISSN: 1535-9476
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal

LANGUAGE: English

AB Increased force generation and smooth muscle remodeling follow the implantation of saphenous vein as an arterial bypass graft. Previously, we characterized and mapped 129 **proteins** in human saphenous vein medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Here, we focus on actin filament remodeling in response to simulated arterial flow. Human saphenous vein was exposed to simulated venous or arterial flow for 90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to 2-**D gel** electrophoresis using a non-linear immobilized pH 3-10 gradient in the first dimension. **Proteins** were analyzed quant. using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 μM) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated **protein** expression (seven paired vein samples). The heat shock **protein** HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance (p = 0.01), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms (p = 0.018). The abundance of actin-capping **protein** α2 subunit CapZ had decreased 3-fold, p = 0.04. A 19-kDa proteolytic fragment of actin increased 2-fold, p = 0.04. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, p = 0.022. The abundance of other **proteins** associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of **proteins** involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005

L1 1052 S @-D GEL
L2 0 S HEAT SKOCK PROTEINS
L3 0 S HEAT SKOCK PROTEIN
L4 0 S CHAPAERONE
L5 15629 S HSP
L6 42 S L1 AND L5
L7 42 S L6 AND PROTEIN
L8 0 S L7 AND PREVENTION AND DENATURATION
L9 0 S L7 AND PREVENTION

=> d L7 1-20 ibib,abs

L7 ANSWER 1 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2005:133528 CAPLUS
DOCUMENT NUMBER: 142:238591
TITLE: Proteomic profiling of human stem cells derived from umbilical cord blood
AUTHOR(S): Zenzmaier, Christoph; Gesslbauer, Bernd; Grobuschek, Nina; Jandrositz, Anita; Preisegger, Karl-Heinz; Kungl, Andreas J.
CORPORATE SOURCE: Lifecord Inc., Graz, A-8010, Austria
SOURCE: Biochemical and Biophysical Research Communications (2005), 328(4), 968-972
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier

DOCUMENT TYPE: Journal
LANGUAGE: English
AB CD34+ prepns. from five different umbilical cord samples were compared with respect to their proteome profile using 2-**D gel** electrophoresis. Fifty-two **protein** spots were found to match in all prepns. referring to the high heterogeneity of such samples indicating a not fully developed (or instable) proteome of stem cells. All matching spots were subjected to in-gel digestion and nano-LC-MS/MS sequence anal., from which 22 **proteins** were unambiguously identified.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1067027 CAPLUS
TITLE: Differential signatures of **protein** expression in marmoset liver and thymus induced by single-dose TCDD treatment
AUTHOR(S): Oberemm, Axel; Meckert, Christine; Brandenburger, Linda; Herzig, Andrea; Lindner, Yvonne; Kalenberg, Kareen; Krause, Eberhard; Ittrich, Carina; Kopp-Schneider, Annette; Stahlmann, Ralf; Richter-Reichhelm, Hans-Bernhard; Gundert-Remy, Ursula
CORPORATE SOURCE: Federal Institute for Risk Assessment, Berlin, 14195, Germany
SOURCE: Toxicology (2005), 206(1), 33-48
CODEN: TXCYAC; ISSN: 0300-483X
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is an ubiquitously distributed environmental pollutant. Health effects have been studied intensively, but low-dose effects are quite complex and not yet fully understood. In many studies, the immune system was identified as the most sensitive target. Here, we demonstrate changes of **protein** expression in liver and thymus of male marmosets (Callithrix jacchus) which were subjected to a single dose of a s.c. injection of 100 ng/kg body weight TCDD. Histopathol. examination revealed myocardial fibrosis, but there were no significant findings in pathol. and histopathol. of liver and thymus. In order to detect more subtle treatment-related changes, we performed a comparative proteomic investigation of liver and thymus using a 2-**D gel** electrophoresis based proteomics approach. Fluorescence labeling and automated image anal. was used to enhance sensitivity and reproducibility. In both organs, distinct changes of **protein** expression were detected which were more pronounced in thymus, where the pattern of deregulated **proteins** could be clearly related to immune responses. In the thymus of treated animals, several toxicol. relevant factors were increased, including chaperones, glycerol-3-phosphate dehydrogenase, and adseverin. Among others, vimentin, Ca-dependent protease and **protein** disulfide isomerase were downregulated. In the liver, transferrins, lamin A and HSP70 were upregulated, whereas thymidine phosphorylase (synonyms: endothelial cell growth factor, PD-ECGF, gliostatin) was significantly reduced. Comparative anal. of deregulated **proteins** in both organs revealed a pattern of related functions, which fits well into the existing knowledge of the toxic processes and mechanisms underlying TCDD-mediated toxicity.
REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1029346 CAPLUS
DOCUMENT NUMBER: 142:110541
TITLE: Proteomic analysis of the response of Arabidopsis chloroplast **proteins** to high light stress

AUTHOR(S): Phee, Bong-Kwan; Cho, Jin-Hwan; Park, Sebyul; Jung, Jin Hee; Lee, Youn-Hyung; Jeon, Jong-Seong; Bhoo, Seong Hee; Hahn, Tae-Ryong
CORPORATE SOURCE: Graduate School of Biotechnology and Plant Metabolism Research Center, Kyung Hee University, Suwon, S. Korea
SOURCE: Proteomics (2004), 4(11), 3560-3568
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 μmol photons·m-2·s-1) conditions and then subjected to high light (1000 μmol photons·m-2·s-1) stress. Chloroplasts were then isolated from these plants and both soluble and insol. **proteins** were extracted and subjected to two-dimensional (2-**D**) **gel** electrophoresis. The resolved **proteins** were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database anal. 64 **Protein** spots, which were identified as candidate factors that responded to high light stress, were then selected for anal. and 52 of these were successfully identified using MALDI-TOF-MS anal. 35 Of the 52 identified **proteins** were found to decrease their expression levels during high light stress and a further 14 of the candidate **proteins** had upregulated expression levels under these conditions. Most of the **proteins** that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated **proteins** were identified as previously well-known high light stress-related **proteins**, such as heat shock **proteins** (**HSPs**), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel **proteins** that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1013025 CAPLUS
DOCUMENT NUMBER: 142:20704
TITLE: Localization of the chaperone **proteins** GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa
AUTHOR(S): Boilard, M.; Reyes-Moreno, C.; Lachance, C.; Massicotte, L.; Bailey, J. L.; Sirard, M.-A.; Leclerc, P.
CORPORATE SOURCE: Departement des Sciences Animales, Centre de Recherche en Biologie de la Reproduction, Universite Laval, Quebec, QC, G1K 7P4, Can.
SOURCE: Biology of Reproduction (2004), 71(6), 1879-1889
CODEN: BIREBV; ISSN: 0006-3363
PUBLISHER: Society for the Study of Reproduction
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of

the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no **protein** candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane exts., either an oviductal factor triggered intracellular events resulting in pos. effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a pos. action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with [35S]-methionine and, upon extensive washes, **proteins** were separated by two-dimensional (2-**D**) **gel** electrophoresis to identify the factors suspected to have beneficial effects on spermatozoa. The six major **proteins**, according to their signal intensity on the autoradiog. film, were extracted from a 2-**D gel** of oviduct epithelial cell **proteins** run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to heat shock **protein** 60 (HSP60) and one to the glucose-regulated **protein** 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these **proteins**. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:767842 CAPLUS
DOCUMENT NUMBER: 142:357
TITLE: Proteomic analysis of **proteins** altered by dibenzoylmethane in human prostatic cancer LNCaP cells
AUTHOR(S): Frazier, Monica C.; Jackson, Kimberly M.; Jankowska-Stephens, Ewa; Anderson, Mark G.; Harris, Wayne B.
CORPORATE SOURCE: CBR/RCMI and Cancer Center, Tuskegee University, Tuskegee, AL, USA
SOURCE: Proteomics (2004), 4(9), 2814-2821
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This paper explores the use of proteomics as a tool for identifying **protein** species whose expression has been altered by dibenzoylmethane (DBM) in LNCaP cells. Although DBM, a constituent of licorice, has been shown to induce cell cycle arrest and regulate androgen receptor (AR) expression, the mechanism by which these events occur is unknown. To develop a better understanding of the effect of DBM on cancer cells, the authors analyzed changes in **protein** expression induced by DBM in LNCaP cells using two-dimensional (2-**D**) **gel** electrophoresis. The proteomic approach used to study LNCaP cells has lead to the anal. and identification of a number of **protein** species that increase or decrease as a result of exposure to DBM. In particular, twenty features were differentially expressed in this study based on the quantitation of two sep. 2-D-fluorescence difference gel electrophoresis analyses. Thirteen of these features were identified through mass spectrometric anal. The intensity of 10 out of the 13 spots identified increased 2- to 3-fold in response to 25 μM and 50 μM DBM and the remaining three spots decreased 2-fold in response to the same DBM treatment. This study investigates proteomic changes induced by treatment of cells with DBM to develop a model for the mechanism by which DBM

induces cell cycle arrest and represses AR expression.
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:637204 CAPLUS
DOCUMENT NUMBER: 141:256616
TITLE: Differential proteomic analysis of intestinal epithelium cell line before and after irradiation by gamma-ray
AUTHOR(S): Zhang, Bo; Su, Yongping; Ai, Guoping; Liu, Xiaohong; Wei, Yongjiang; Wang, Fengchao; Cheng, Tianmin
CORPORATE SOURCE: College of Preventive Medicine, Third Military Medical University, Chongqing, 400038, Peop. Rep. China
SOURCE: Di-San Junyi Daxue Xuebao (2003), 25(24), 2157-2160
CODEN: DYXUE8; ISSN: 1000-5404
PUBLISHER: Di-San Junyi Daxue Xuebao Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB Study the **proteins** associated with ionizing irradiation of intestinal epithelium cell line (IEC-6), and elucidate the mol. mechanism of reconstruction of intestinal epithelium damaged by ionizing irradiation **Protein** samples extracted from normal IEC-6 cells and IEC-6 cells irradiated by γ-ray at the dose of 25 Gy were separated by immobilized pH gradient two-dimensional (2-**D**) **gel** electrophoresis. After Coomasie blue staining, the 2-D electrophoretogram was analyzed using PDQuest software. The differential **proteins** were cut off from the Coomasie-blue stained gel and digested in gel with trypsin, and then identified by peptide mass fingerprinting based on matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) and database searching. Total RNA of IEC-6 cells was isolated and RT-PCR anal. was performed using primers of ERP29 and GAPDH. After Coomasie blue staining, the 2-DE image anal. by PDQuest software detected (608±39) spots in normal IEC-6 cell sample and (595 ± 31) spots in irradiated cells, of which 396 spots were matched. Sixteen differential spots were cut off from the Coomasie blue stained gel, and 11 spots were preliminarily identified. These **proteins** were associated with cell metabolism, cytoskeleton, and free radical elimination, etc.
Ionizing radiation induced mRNA of ERP29 in a time-dependent manner over a 48-h period. The results indicated that γ-ray irradiation can induce changes of the **protein** expression pattern of intestinal epithelium cell line. This helps to understand the mol. mechanisms of ionizing radiation on intestinal epithelium cells.

L7 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:579538 CAPLUS
DOCUMENT NUMBER: 141:222844
TITLE: Heat shock **protein** 70 (Hsp70) subtype expression in neuroendocrine tissue and identification of a neuroendocrine tumour-specific Hsp70 truncation
AUTHOR(S): Zierhut, B.; Mechtler, K.; Gartner, W.; Daneva, T.; Base, W.; Weissel, M.; Niederle, B.; Wagner, L.
CORPORATE SOURCE: Department of Medicine III, Division of Clinical Endocrinology and Metabolism, University of Vienna, Vienna, A-1090, Austria
SOURCE: Endocrine-Related Cancer (2004), 11(2), 377-389
CODEN: ERCAE9; ISSN: 1351-0088
PUBLISHER: Society for Endocrinology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In order to identify neuroendocrine tumor-specific **protein** expression, we generated monoclonal antibodies (mAbs) with a tumor-related reaction pattern using a human insulinoma as immunogen. One of the

generated mAbs (mAb 1D4) exhibited striking immunoreactivity against various neuroendocrine tumors without staining pancreatic islets of Langerhans. Furthermore, mAb 1D4 immunostained a characteristic subtype of hypothalamic neurons. Using two-dimensional (2-**D**) **gel** electrophoresis, mAb 1D4 immunoblotting and mass spectrometry, heat shock **protein** 70 (Hsp70) isoforms were identified as the mAb 1D4-specific antigen. In hypothalamic tissue, the presence of two different Hsp70 isoforms (Hsp70-8 and Hsp70-1) was revealed by 2-**D** **gel** immunoblots and consecutive mass spectrometric peptide anal. In contrast, insulinoma and other neuroendocrine tumors displayed solely Hsp70-8 expression. Moreover, the tumor-specific presence of an addnl. mAb 1D4 immunoreactive **protein** of 40 kDa was observed in eight out of eight tested neuroendocrine tumors. For this variant, exclusively, peptides derived from the C terminus excluding the 299 amino-terminal residues were detected. In cultured tumor-derived fibroblasts, expression of the truncated Hsp70-8 subtype was not present. In conclusion, we have demonstrated a neuroendocrine tumor-specific expression pattern of Hsp70 isoforms and identified an as yet unknown N-terminally truncated Hsp70-8 variant.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:576084 CAPLUS
DOCUMENT NUMBER: 141:257757
TITLE: The proteome of chicken skeletal muscle: Changes in soluble **protein** expression during growth in a layer strain
AUTHOR(S): Doherty, Mary K.; McLean, Lynn; Hayter, Julia R.; Pratt, Julie M.; Robertson, Duncan H. L.; El-Shafei, Abdel; Gaskell, Simon J.; Beynon, Robert J.
CORPORATE SOURCE: Protein Function Group, Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, L69 7ZJ, UK
SOURCE: Proteomics (2004), 4(7), 2082-2093
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The whole animal, and the pectoralis muscle in particular, grows at a greatly enhanced rate in chickens selected for meat production (broilers) when compared to those selected for egg production (layers). As part of an ongoing study to analyze muscle **protein** dynamics under conditions of rapid growth, the authors have embarked upon a preliminary characterization of the proteome of layer chicken pectoralis muscle, at specified time-points from 1 to 27 days after hatching. Soluble exts. of muscle homogenates were separated by two-dimensional (2-**D**) **gel** electrophoresis and selected spots were analyzed by in-gel tryptic digestion and matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry. Of 90 spots, 51 gave mass spectra that matched to existing chicken **proteins** present in online databases, 12 matched equivalent **proteins** from non-avian species and 11 yielded good quality spectra but were unable to be matched against existing databases. For many of these **proteins**, growth over 27 days elicited dramatic changes in relative expression levels. Chicken skeletal muscle offers an excellent system for developmental proteomics.
REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:328454 CAPLUS
DOCUMENT NUMBER: 140:421867
TITLE: Nuclear matrix **protein** expressions in hepatocytes of normal and cirrhotic rat livers under

normal and regenerating conditions
AUTHOR(S): Yun, Jing-Ping; Liew, Choong-Tsek; Chew, Eng Ching; Yin, Xiao-Yu; Lai, Paul Bo San; Fai, Yam Hin; Li, H. K. Richard; Jin, Mei-Lin; Ding, Ming-Xiao; Li, Ming-Tao; Lin, Han-Liang; Lau, Wan Yee
CORPORATE SOURCE: Department of Pathology, Cancer Center of Sun Yat-Sen University, Guangzhou, 510060, Peop. Rep. China
SOURCE: Journal of Cellular Biochemistry (2004), 91(6), 1269-1279
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We explored the feasibility of studying nuclear matrix **protein** (NMP) expressions of the hepatocytes in normal and cirrhotic rat livers with liver regeneration after partial hepatectomy. Sixteen Wistar healthy rats were studied with exptl. liver regeneration and/or liver cirrhosis. Two-dimensional (2-**D**) **gel** electrophoresis was used to generate these NMP compns. from these rat liver samples. Several antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and heat shock **protein** 70 were used for identification by Western blot. Totally, 41 strongly stained **protein** spots were characterized on the 2-**D gels**. Thirty-four **protein** spots were detected in all of these rat livers, of which, cytokeratin, vimentin, actin, HNF4α, and heat shock **protein** 70 were identified. B23 was detected in the regenerated livers. Three **protein** spots (s33, s34, and s35) were detectable only in NMP preparation extracted from the regenerating rat livers after hepatectomy. Another 3 **protein** spots (s36, s37, and s38) were detectable only in NMP preparation extracted from thioacetamide-induced cirrhotic rat livers. Under these conditions including exptl. liver regeneration and/or liver cirrhosis, Over thirty higher abundance NMPs of hepatocytes were consistently expressed and considered as common and basic NMPs. Some of the NMPs are specific for liver regeneration and may play a critical role in cell proliferation and cell cycle, and some are specific for liver cirrhosis.
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:161172 CAPLUS
DOCUMENT NUMBER: 140:284961
TITLE: F-actin capping (CapZ) and other contractile saphenous vein smooth muscle **proteins** are altered by hemodynamic stress: A proteomic approach
AUTHOR(S): McGregor, Emma; Kempster, Lee; Wait, Robin; Gosling, Martin; Dunn, Michael J.; Powell, Janet T.
CORPORATE SOURCE: Department of Vascular Surgery, Imperial College School of Medicine at Charing Cross Hospital, London, W6 8RP, UK
SOURCE: Molecular and Cellular Proteomics (2004), 3(2), 115-124
CODEN: MCPOBS; ISSN: 1535-9476
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Increased force generation and smooth muscle remodeling follow the implantation of saphenous vein as an arterial bypass graft. Previously, we characterized and mapped 129 **proteins** in human saphenous vein medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Here, we focus on actin filament remodeling in response to simulated arterial flow. Human saphenous vein was exposed to simulated venous or arterial flow for

90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to 2-**D gel** electrophoresis using a non-linear immobilized pH 3-10 gradient in the first dimension. **Proteins** were analyzed quant. using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 μM) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated **protein** expression (seven paired vein samples). The heat shock **protein** HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance ($p = 0.01$), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms ($p = 0.018$). The abundance of actin-capping **protein** α2 subunit CapZ had decreased 3-fold, $p = 0.04$. A 19-kDa proteolytic fragment of actin increased 2-fold, $p = 0.04$. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, $p = 0.022$. The abundance of other **proteins** associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of **proteins** involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:73404 CAPLUS

DOCUMENT NUMBER: 140:332868

TITLE: Phosphoproteome Analysis of Cardiomyocytes Subjected to β-Adrenergic Stimulation. Identification and characterization of a cardiac heat shock **protein** p20

AUTHOR(S): Chu, Guoxiang; Egnaczyk, Gregory F.; Zhao, Wen; Jo, Su-Hyun; Fan, Guo-Chang; Maggio, John E.; Xiao, Rui-Ping; Kranias, Evangelia G.

CORPORATE SOURCE: Department of Pharmacology & Cell Biophysics, University of Cincinnati College of Medicine, Cincinnati, OH, USA

SOURCE: Circulation Research (2004), 94(2), 184-193
CODEN: CIRUAL; ISSN: 0009-7330

PUBLISHER: Lippincott Williams & Wilkins

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Posttranslational modification of target substrates underlies biol. processes through activation/inactivation of signaling cascades. To concurrently identify the phosphoprotein substrates associated with cardiac β-adrenergic signaling, the mouse myocyte phosphoproteome was analyzed using 2-**D gel** electrophoresis in combination with 32P autoradiog. Phosphoprotein spots, detected by silver staining, were identified using MALDI-TOF mass spectrometry in conjunction with computer-assisted **protein** spot matching. Stimulation with isoproterenol (1 μmol/L for 5 min) was associated with maximal increases in myocyte contractile parameters, and significant stimulation of the phosphorylation of troponin I (190±23%) and succinyl CoA synthetase (160±16%), whereas the phosphorylation of pyruvate dehydrogenase (48±10%), NADH-ubiquinone oxidoreductase (46±6%), heat shock **protein** 27 (18±3%), αB-crystallin (20±3%), and an unidentified 26-kDa **protein** (29±7%) was significantly decreased, compared with unstimulated cells (100%). After sustained (30 min) stimulation with isoproterenol, only the alterations in the phosphorylation levels of troponin I and NADH-ubiquinone oxidoreductase were maintained and de novo phosphorylation of a phosphoprotein (≈20 kDa and pI 5.5) was observed The tryptic peptide fragments of this phosphoprotein were sequenced using postsource decay mass

spectrometry, and the **protein** was subsequently cloned and designated as p20, based on its high sequence homol. with rat and human skeletal p20. The mouse cardiac p20 contains the conserved domain sequences for heat shock **proteins**, and the RRAS consensus sequence for cAMP-PKA substrates. LC-MS/MS phosphorylation mapping confirmed phosphorylation of Ser16 in p20 on β-agonist stimulation. Adenoviral gene transfer of p20 was associated with significant increases in contractility and Ca transient peak in adult rat cardiomyocytes, suggesting an important role of p20 in cardiac function. These findings suggest that cardiomyocytes undergo significant posttranslational modification via phosphorylation in a multitude of **proteins** to dynamically fine-tune cardiac responses to β-adrenergic signaling.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:786668 CAPLUS
DOCUMENT NUMBER: 140:38508
TITLE: Surface localized heat shock **protein** 20 (HslV) of Helicobacter pylori
AUTHOR(S): Du, Rui Juan; Ho, Bow
CORPORATE SOURCE: Department of Microbiology, National University of Singapore, Singapore, 117597, Singapore
SOURCE: Helicobacter (2003), 8(4), 257-267
CODEN: HELIFL; ISSN: 1083-4389
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Heat Shock **Protein** (**HSP**) has been regarded as a pathogenic factor in Helicobacter pylori infection. Heat Shock **Protein** 20 (HSP20) of H. pylori is identified as HslV based on open reading frame predication of genome sequences. It is a homolog of HslV of E. coli, a peptidase involved in **protein** degradation The HSP20 gene was cloned and inserted into pET16b fused with His-tag. Recombinant HSP20 **protein** (rHSP20) was expressed and purified by nickel column. Rabbit anti-rHSP20 was purified by **Protein** A affinity chromatog. and used as a probe to localize HSP20 in H. pylori by immuno-gold labeling and Western blotting. RHSP20 was also used as antigen to test for antibody against HSP20 in patients with H. pylori infection by ELISA. Immuno-gold labeled transmission electron microscopy shows that HSP20 is located on the cell surface of H. pylori. Western blotting of 2-**D** **gel** shows that HSP20 has a pI of .apprx.5.5 and a mol. weight of .apprx.18 kDa. The ELISA result shows that there is no significant difference in antibody titer against rHSP20 in all sera tested. The presence of IgG to rHSP20 may imply an earlier exposure of the patients and normal subjects to H. pylori. However, the mechanism has not been established. HSP20 has been shown to localize on the surface of H. pylori. Surface localization of H. pylori HSP20 may provide the path to a better understanding of the role and function of HSP20 in bacteria-host interaction.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:756715 CAPLUS
DOCUMENT NUMBER: 139:319795
TITLE: Developmentally induced changes of the proteome in the protozoan parasite Leishmania donovani
AUTHOR(S): Bente, Meike; Harder, Simone; Wiesgigl, Martina; Heukeshoven, Jochen; Gelhaus, Christoph; Krause, Eberhard; Clos, Joachim; Bruchhaus, Iris
CORPORATE SOURCE: Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany
SOURCE: Proteomics (2003), 3(9), 1811-1829

CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In order to proceed through their life cycle, protozoan parasites of the genus Leishmania cycle between sandflies and mammals. This change of environment correlates with the differentiation from the promastigote stage (insect form) to the amastigote stage (intracellular mammalian form). The mol. basis underlying this major transformation is poorly understood so far; however, heat shock **protein** 90 (HSP90) appears to play a pivotal role. To further elucidate this process we identified **proteins** expressed preferentially in either of the two life cycle stages. By using two-dimensional (2-**D**) **gel** electrophoresis we observed defined changes in the **protein** pattern. A total of approx. 2000 **protein** spots were visualized. Of these, 31 **proteins** were present only in promastigotes. The abundance of 65 **proteins** increased during heat-induced in vitro amastigote differentiation, while a decreased abundance is observed for four **proteins** late in amastigote differentiation. Further analyses using matrix-assisted laser desorption/ionization-time of flight mass spectrometry and peptide mass fingerprinting 67 **protein** spots were identified representing 41 different **proteins** known from databases and eight hypothetical **proteins**. Further studies showed that most of the stage-specific **proteins** fall into five groups of functionally related **proteins**. These functional categories are: (i) stress response (e.g. heat, oxidative stress); cytoskeleton and cell membrane; (iii) energy metabolism and phosphorylation; (iv) cell cycle and proliferation; and (v) amino acid metabolism Very similar changes in the 2-D **protein** pattern were obtained when in vitro amastigote differentiation was induced either by pharmacol. inhibition of HSP90 or by a combination of heat stress and acidic pH supporting the critical role for HSP90 in life cycle control.
REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:187666 CAPLUS
DOCUMENT NUMBER: 138:352824
TITLE: Identification of cellular changes associated with increased production of human growth hormone in a recombinant chinese hamster ovary cell line
AUTHOR(S): Van Dyk, Derek D.; Misztal, David R.; Wilkins, Marc R.; Mackintosh, James A.; Poljak, Anne; Varnai, Jodie C.; Teber, Erdahl; Walsh, Bradley J.; Gray, Peter P.
CORPORATE SOURCE: Australian Proteome Analysis Facility, Macquarie University, Sydney, 2109, Australia
SOURCE: Proteomics (2003), 3(2), 147-156
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A proteomics approach was used to identify the **proteins** potentially implicated in the cellular response concomitant with elevated production levels of human growth hormone in a recombinant Chinese hamster ovary (CHO) cell line following exposure to 0.5 mM butyrate and 80 μM zinc sulfate in the production media. This involved incorporation of two-dimensional (2-**D**) **gel** electrophoresis and **protein** identification by a combination of N-terminal sequencing, matrix-assisted laser desorption/ionization-time of flight mass spectrometry, amino acid anal. and cross species database matching. From these identifications a CHO 2-D reference map and annotated database have been established. Metabolic labeling and subsequent autoradiog. showed the induction of a number of cellular **proteins** in response to the media

additives butyrate and zinc sulfate. These were identified as GRP75, enolase and thioredoxin. The chaperone **proteins** GRP78, HSP90, GRP94 and HSP70 were not up-regulated under these conditions.

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:102809 CAPLUS
DOCUMENT NUMBER: 136:212531
TITLE: Small heat shock **protein** p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells
AUTHOR(S): Willsie, Julia K.; Clegg, James S.
CORPORATE SOURCE: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA
SOURCE: Journal of Cellular Biochemistry (2001), 84(3), 601-614
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The small heat shock/α-crystallin **protein** p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp Artemia franciscana. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other **HSPs** in stabilizing nuclear matrix **proteins** (NMPs), nuclear matrixes from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional (2-**D**) **gel** electrophoresis and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix prepns. from control and heat-shocked embryos showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

REFERENCE COUNT: 101 THERE ARE 101 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:689424 CAPLUS
DOCUMENT NUMBER: 135:353186
TITLE: Proteome alterations in human hepatoma cells transfected with antisense epidermal growth factor receptor sequence
AUTHOR(S): Yu, Li-Rong; Shao, Xiao-Xia; Jiang, Wan-Li; Xu, Dan; Chang, Yun-Chao; Xu, Yong-Hua; Xia, Qi-Chang
CORPORATE SOURCE: Research Center for Proteome Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, 200031, Peop. Rep. China
SOURCE: Electrophoresis (2001), 22(14), 3001-3008
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The epidermal growth factor (EGF) is a member of the growth factor superfamily that can stimulate the proliferation of many types of cells.

Overexpression of EGF receptor (EGFR) was observed in many types of cancer cells. Anti-EGFR antibodies or antisense nucleic acid sequences of EGFR can suppress the growth of hepatoma cells. In order to further investigate the proteome alterations associated with malignant growth of the human hepatoma cells and the influence of EGFR signal pathway on the cellular proteome, the authors have comparatively analyzed the proteomes of human hepatoma cells transfected with antisense EGFR sequence (cell strain JX-1) and its control cells (cell strain JX-0) by two-dimensional (2-**D**) **gel** electrophoresis and mass spectrometry. Image anal. of silver-stained 2-**D gels** revealed that 40 **protein** spots showed significant expression changes in JX-1 cells compared to JX-0 cells. Three of them, including the tumor suppressor **protein** maspin, changed with tendency to the normal levels. Two **protein** spots were identified as HSP27 in the same gel, and one of them had a reduced level in JX-1 cells. The apparent alterations of HSP27 in expression level might be the results from their differential chemical modifications, suggesting the effect of dynamic post-translational modifications of **proteins** on the growth of hepatoma cells. Other **proteins** such as glutathione peroxidase (GPX-1) and 14-3-3-sigma also exhibited altered expression in JX-1 cells, and their functional implications are discussed.

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 17 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:527698 CAPLUS

DOCUMENT NUMBER: 136:180356

TITLE: Modification of the **protein** expression pattern induced in the nitrogen-fixing actinomycete Frankia sp. strain ACN14a-tsr by root exudates of its symbiotic host Alnus glutinosa and cloning of the sodF gene

AUTHOR(S): Hammad, Y.; Marechal, J.; Cournoyer, B.; Normand, P.; Domenach, A.-M.

CORPORATE SOURCE: Ecologie Microbienne. UMR CNRS 5557, Universite LYON 1, Villeurbanne, 69622, Fr.

SOURCE: Canadian Journal of Microbiology (2001), 47(6), 541-547
CODEN: CJMIAZ; ISSN: 0008-4166

PUBLISHER: National Research Council of Canada

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Two-dimensional (2-D) polyacrylamide gel electrophoresis was used to detect **proteins** induced in Frankia sp. strain ACN14a-tsr by root exudates of its symbiotic host, Alnus glutinosa. The 5 most prominent **proteins** were purified from 2-**D gels** and characterized by N-terminal sequencing. All of these **proteins** had a high percentage of similarity with known stress **proteins**. One **protein** match was the Fe superoxide dismutase (Fe-SOD), another was a tellurite resistance **protein** (Ter), the third was a bacterioferritin comigratory **protein** (Bcp): and two matches, differing only by their isoelec. point, were the same small heat shock **protein** (**Hsp**), a major immune reactive **protein** found in mycobacteria. This suggests that the symbiotic microorganism Frankia, first responds with a normal stress response to toxic root products of its symbiotic host plant. To confirm its identity, the gene corresponding to the Fe-SOD **protein**, sodF was isolated from a genomic library by a PCR-approach and sequenced. It is the first stress response gene characterized in Frankia.

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:362017 CAPLUS

DOCUMENT NUMBER: 135:90969
TITLE: The reduction of NADH ubiquinone oxidoreductase 24- and 75-kDa subunits in brains of patients with Down syndrome and Alzheimer's disease
AUTHOR(S): Kim, Seong Hwan; Vlkolinsky, Roman; Cairns, Nigel; Fountoulakis, Michael; Lubec, Gert
CORPORATE SOURCE: Department of Pediatrics, University of Vienna, Vienna, A-1090, Austria
SOURCE: Life Sciences (2001), 68(24), 2741-2750
CODEN: LIFSAK; ISSN: 0024-3205
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB NADH:ubiquinone oxidoreductase (complex I), one of the most complicated multi-**protein** enzyme complexes, is important for energy metabolism because it is the initial enzyme of the mitochondrial respiratory chain. Deficiency of complex I is frequently found in various tissues of patients with neurodegenerative disease. Here we studied the **protein** levels of complex I 24- and 75-kDa subunits in several brain regions from patients with Down syndrome (DS) and Alzheimer's disease (AD). We determined **protein** levels of complex I 24-, 75-kDa subunits and mitochondrial marker **proteins** mitochondrial matrix **protein** P1 (hsp60) and aconitate hydratase from seven brain regions of patients with DS, AD and controls. **Proteins** were separated by two-dimensional (2-**D**) **gel** electrophoresis and identified by matrix-assisted laser desorption ionization mass spectrometry (MALDI-MS). Complex I 24-kDa subunit was significantly reduced in occipital cortex and thalamus in patients with DS and temporal and occipital cortices in patients with AD. Complex I 75-kDa subunit was significantly reduced in brain regions from patients with DS (temporal, occipital and caudate nucleus) and AD (parietal cortex). Redns. of two subunits of complex I may lead to the impairment of energy metabolism and result in neuronal cell death (apoptosis), a hallmark of both neurodegenerative disorders.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2000:659286 CAPLUS
DOCUMENT NUMBER: 133:361412
TITLE: Identification of differentially expressed **proteins** between human hepatoma and normal liver cell lines by two-dimensional electrophoresis and liquid chromatography-ion trap mass spectrometry
AUTHOR(S): Yu, Li-Rong; Zeng, Rong; Shao, Xiao-Xia; Wang, Nan; Xu, Yong-Hua; Xia, Qi-Chang
CORPORATE SOURCE: Shanghai Institute of Biochemistry, Chinese Academy of Sciences, Shanghai, 200031, Peop. Rep. China
SOURCE: Electrophoresis (2000), 21(14), 3058-3068
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In the previous study, the proteomes of the human hepatoma cell line BEL-7404 and the normal human liver cell line L-02 were separated by high resolution two-dimensional electrophoresis (2-DE). Image anal. revealed that 99 **protein** spots showed quant. and qual. variations that were significant ($P < 0.01$) and reproducible. Here we report the identification results of some of these **protein** spots. **Protein** spots excised from 2-**D gels** were subjected to in-gel digestion with trypsin, and the resulting peptides were measured by microbore high performance liquid chromatog. - ion trap - mass spectrometry (LC-IT-MS) to obtain the tandem mass (MS/MS) spectra. Twelve **protein** spots were identified with high confidence using SEQUEST with uninterpreted MS/MS raw data. Besides inosine-5'-

monophosphate dehydrogenase 2, heat shock 27 kDa **protein**, calreticulin and calmodulin, whose expression was elevated in hepatoma cells, glutathione-S-transferse P was identified from hepatoma cells in which its level was 18-fold higher compared to human liver cells. Two spots were identified as the homologs of reticulocalbin for the first time in hepatoma cells and their expression increased compared to liver cells. However, tubulin beta-1 chain and natural killer cell enhancing factor B were downregulated in hepatoma cells. A tumor suppressing serpin, maspin precursor, was identified from one spot whose quantity was much higher in the normal liver cell line. More interestingly, epidermal fatty acid-binding **protein** (E-FABP) and fatty acid-binding **protein**, adipocyte-type (A-FABP), were detected in liver cells but not in hepatoma cells. The functional implication of the identified **proteins** was discussed.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:228153 CAPLUS

DOCUMENT NUMBER: 132:332111

TITLE: Changes in **protein** synthesis and phosphorylation during microspore embryogenesis in Brassica napus

AUTHOR(S): Cordewener, Jan; Bergervoet, Jan; Liu, Chun-Ming

CORPORATE SOURCE: Plant Research International, Wageningen, 6700 AA, Neth.

SOURCE: Journal of Plant Physiology (2000), 156(2), 156-163
CODEN: JPPHEY; ISSN: 0176-1617

PUBLISHER: Urban & Fischer Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Changes in **protein** synthesis and phosphorylation during microspore embryogenesis in Brassica napus were investigated by two-dimensional (2-**D**) **gel** electrophoresis. The expression pattern of 6 **proteins** previously identified as putative markers for embryo initiation in microspore cultures was studied during later stages of embryo development. All of them were transiently expressed for the induction period (8 h to 2 days) and disappeared on the 5th day but two of them were expressed again at the later stage of embryogenesis (12th day). Major changes in the patterns of **protein** synthesis were observed 5 days after initiation of microspore embryogenesis. In this period of time embryogenic microspores have formed proembryos within their exine. Later stages of embryo development were not accompanied by major changes in 2-D **protein** patterns. Comparison of 2-D patterns of phosphorylated **proteins** revealed minor differences between embryogenic and non-embryogenic cultures, except for the level of phosphorylation of hsp70. A clear difference of extracellular secreted **proteins** was observed between embryogenic and non-embryogenic microspore cultures. This work provides a biochem. insight for the understanding of microspore embryogenesis at the **protein** level.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

File 5:Biosis Previews(R) 1969-2005/Apr W2
(c) 2005 BIOSIS

```
      Set  Items  Description
      ---  -----  -----------
? s heat()shock()protein?
         132844  HEAT
          91472  SHOCK
        1712861  PROTEIN?
      S1  21855  HEAT()SHOCK()PROTEIN?
? s electrophoresis and s1
         196277  ELECTROPHORESIS
          21855  S1
      S2   1259  ELECTROPHORESIS AND S1
? s (2()D()electrophoresis) and s1
        3182451  2
         729009  D
         196277  ELECTROPHORESIS
            276  2(W)D(W)ELECTROPHORESIS
          21855  S1
      S3      9  (2()D()ELECTROPHORESIS) AND S1
? t s3/7/1-9
```

KEC 4-14-05

3/7/1
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015163322 BIOSIS NO.: 200500070387
Characterization of particulate proteins in Pacific surface waters
AUTHOR: Saijo Sachiko; Tanoue Eiichiro (Reprint)
AUTHOR ADDRESS: Grad Sch Environm StudiesDept Earth and Environm SciChikusa Ku, Nagoya Univ, Furo Cho, Nagoya, Aichi, 4648601, Japan**Japan
AUTHOR E-MAIL ADDRESS: tanoue@ihas.nagoya-u.ac.jp
JOURNAL: Limnology and Oceanography 49 (4): p953-963 July 2004 2004
MEDIUM: print
ISSN: 0024-3590 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We investigated molecular characteristics of particulate proteins in Pacific surface waters using two-dimensional electrophoresis (2DE). Most proteinaceous materials estimated by dye-binding methods were characterized by the 2DE unresolved acidic materials with a broad range of molecular mass and the 2DE unresolved low molecular mass materials with a broad range of isoelectric point. The 2DE unresolved acidic and low molecular mass materials were considered to comprise peptides conjugated with acidic saccharides and degradation products (peptides) of proteins, respectively, which indicates that almost all proteins in living organisms failed to survive in detrital particulate organic matter (POM). Nevertheless, 23 discrete proteins were distinguished by the 2DE. Electrophoretic patterns of the discrete proteins indicated that they were a component of detrital POM. Three discrete proteins were subjected to N terminal amino acid sequence analysis. Two proteins out of three could not be determined because their N termini were blocked, and one protein was determined from the N terminus to the ninth amino acid residue. A homology search revealed that the N terminal amino acid

sequence of the protein agreed completely with that of 70 kDa %%%heat%%% %%%shock%%% %%%protein%%% (HSP70) derived from photosynthetic organisms. HSP70 is a major member of the molecular chaperones that protect or repair proteins from damage under conditions of environmental stress. The occurrence of HSP70 in this study demonstrated that phytoplankton were able to induce the molecular chaperone(s). Clarification of factor(s) controlling induction of chaperones will enable us to assess the actual environmental stress on phytoplankton at the biomolecular level.

3/7/2
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014657598 BIOSIS NO.: 200400028355
Characterization of spermatozoa surface antigens by antisperm antibodies and its influence on acrosomal exocytosis.
AUTHOR: Bohring Claudia (Reprint); Krause Walter
AUTHOR ADDRESS: Andrology, Deutschhausstrasse 9, D-35033, Marburg, Germany **Germany
AUTHOR E-MAIL ADDRESS: bohring@mailer.uni-marburg.de
JOURNAL: American Journal of Reproductive Immunology 50 (5): p411-419 November 2003 2003
MEDIUM: print
ISSN: 1046-7408 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: PROBLEM: Antisperm antibodies (ASA) are the main cause of immunological infertility, they impair sperm functions by binding to the sperm membrane. The aim of this study was to characterize highly enriched sperm membrane proteins by %%%2%%%-%%%D%%%-%%%electrophoresis%%% and to identify membrane antigens binding ASA and to evaluate the influence of ASA on the acrosome reaction (AR). METHOD OF STUDY: Sperm membrane proteins were separated by %%%2%%%-%%%D%%%-%%%electrophoresis%%% and antigens were identified by immunoblotting with ASA from seminal plasma samples of infertile men. The influence of ASA on the AR were observed and determined by means of flowcytometry. RESULTS: A total of 18 antigens were identified by using ASA from seminal plasma. Six of the recognized proteins were analyzed by means of mass spectrometry and peptide matching: HSP70 and HSP70-2, disulfide-isomerase-ER60, caspase-3 and two subunits of the proteasome (component-C2 and zeta-chain). ASA from seminal plasma are able to enhance the AR in donor-spermatozoa. CONCLUSION: The biochemical identification of these proteins will be helpful to understand the mechanism by which ASA impair sperm function and the fertilization process. Spermatozoa, in which the AR was prematurely induced by ASA, will not be able to fertilize anymore.

3/7/3
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014501924 BIOSIS NO.: 200300470643
The proteomics approach to find biomarkers in gastric cancer.
AUTHOR: Ryu Jin-Woo; Kim Hyung-jee (Reprint); Lee Young-Sun; Myong Na-Hye;

Hwang Cheol-Hoh; Lee Gae-Sung; Yom Heng-Cherl
AUTHOR ADDRESS: Department of Urology, College of Medicine, Dankook University, San-29 Anseo-dong, Cheonan, 330-714, South Korea**South Korea
AUTHOR E-MAIL ADDRESS: killtumor@yahoo.co.kr
JOURNAL: Journal of Korean Medical Science 18 (4): p505-509 August 2003 2003
MEDIUM: print
ISSN: 1011-8934
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Gastric cancer is a very serious disease and is naturally resistant to many anticancer drugs. To reduce the mortality and improve the effectiveness of therapy, many studies have tried to find key biomarkers. Proteomic technologies are providing the tools needed to discover and identify disease-associating biomarkers. The proteomic study of gastric cancer establishes any specific events that lead to cancer, and it provides a direct way to define the true function of genes. Using two dimensional (%%%2%%%-%%%D%%%) %%%electrophoresis%%% of the stomach cancer tissue, we have gained about 1,500 spots in each gel, and 140 protein spots also were identified. Among the identified proteins, there were seven over-expressed proteins in stomach cancer tissue: NSP3, transgelin, prohibitin, %%%heat%%% %%%shock%%% %%%protein%%% (hsp) 27 and variant, protein disulfide isomerase A3, unnamed protein product and glucose regulated protein. There were also seven under-expressed proteins in stomach cancer: Apolipoprotein A-1, p20, nucleoside diphosphate isomerase A, alpha 1 antitrypsin, desmin, serum albumin and serotransferrin.

3/7/4
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014299988 BIOSIS NO.: 200300258632
Effect of cigarette smoking on endothelial cells: a proteomic approach.
AUTHOR: Raveendran M (Reprint); Wang J; Utama B; Dudley D; Wang X L
AUTHOR ADDRESS: Genetics, SW Fnd for Biomed Res, 7620 NW Loop 410, San Antonio, TX, 78227-5301, USA**USA
AUTHOR E-MAIL ADDRESS: mraveend@darwin.sfbr.org; jwang@darwin.sfbr.org; autama@darwin.sfbr.org; dudleyd@uthscsa.edu; xwang@darwin.sfbr.org
JOURNAL: FASEB Journal 17 (4-5): pAbstract No. 412.1 March 2003 2003
MEDIUM: e-file
CONFERENCE/MEETING: FASEB Meeting on Experimental Biology: Translating the Genome San Diego, CA, USA April 11-15, 2003; 20030411
SPONSOR: FASEB
ISSN: 0892-6638 _(ISSN print)
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We observe that cigarette smoking causes endothelial dysfunction by inducing excess apoptosis, and the effect can be partially protected by prior eNOS activation. In this study, we systemically investigated protein changes in cigarette smoke extract (CSE) treated endothelial cells using a proteomic approach. HUVEC were treated with 0.01 cigarette

equivalents/ml CSE for 24hrs, with or without preconditioning by L-Arg (400(M, substrate for eNOS) or L-NAME (200(M, NOS inhibitor). Proteins were then harvested for %%%2%%%-%%%D%%% %%%electrophoresis%%% (O'Farrell method). The silver stained gels were scanned with a laser densitometer and subjected to computer analysis. The proteins with more than 4 fold changes were analyzed by MALDI-MS and matched with the profile of known proteins. To confirm the result the change in the protein level was also crosschecked by western blot. We were able to detect 325 proteins by silver staining after %%%2%%%-%%%D%%% %%%electrophoresis%%%. Among those, 33 proteins had more than 3 fold increases or decreases and 15 proteins had more than 4 fold changes when comparing the CSE treated with the control cells. HSP-70-Lamin B1, HSP-70, HSP 27, Alpha-actinin, Annexin 6, Annexin 2, Moesin, HSP gp96 and Laminin-binding protein were up regulated. Myosin light chain, Prolyl 4-hydroxylase, eIF4A, Alpha enolase, Alpha tubulin, and Alpha tubulin Glutaminase were down regulated.)The identified proteins represent several different pathways including the apoptosis and stress response to CSE exposure. This unbiased systemic approach provides more insights into the mechanisms mediating the biological effects by cigarette smoking.

3/7/5
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014014727 BIOSIS NO.: 200200608238
Identification of iron-regulated outer membrane proteins of Mannheimia haemolytica by comparative %%%2%%%-%%%D%%% %%%electrophoresis%%%, Western blotting, and MALDI-TOF
AUTHOR: Zehr E S (Reprint); Tabatabai L B (Reprint); Frank G H (Reprint)
AUTHOR ADDRESS: Natl. Animal Disease Ctr., USDA, ARS, Ames, IA, USA**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 102 p286 2002 2002
MEDIUM: print
CONFERENCE/MEETING: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002; 20020519
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Background: Mannheimia haemolytica(MH) inhabits the tonsils and nasal passages of healthy cattle as a small portion of the normal bacterial flora. After transport or during viral-induced illnesses, MH serotype A1 can undergo a rapid, selective growth in the nasopharynx, and proceed to cause acute pneumonia. Vaccination with MH possessing expressed iron-regulated outer membrane proteins (IROMPs) has inhibited colonization of the nasopharynx. In vaccinated cattle, antibodies to IROMPs correlated with inhibition of MH colonization. A common mechanism for pathogens to obtain iron from the host is to up-regulate iron acquisition proteins. To study the role of IROMPs in colonization of the nasopharynx, IROMPs were isolated and identified. Methods: OMPs from MH grown in iron-restricted (brain heart infusion broth containing 2,2'-dipyridyl) and in iron-replete broth were treated with DNase and RNase, then precipitated with trichloroacetic acid. OMPs were subjected to %%%2%%%-%%%D%%% %%%electrophoresis%%% and compared using BioRad's

PD-Quest software. OMPs that were up-regulated in the iron-restricted medium (presumably IROMPs) were determined to be nonimmunoreactive or immunoreactive by Western blotting using convalescent bovine antiserum as a probe. Selected IROMPs were picked from gels, digested with trypsin, and analyzed by MALDI-TOF for identification using Prospector's MS-FIT software. Results: Thus far, two of the selected immunoreactive IROMPs have been identified as transferrin binding proteins, TbpA and TbpB. Additional up-regulated proteins are homologous to the TonB receptor, %%%heat%%% %%%shock%%% %%%proteins%%%, and transcription regulators of several bacterial species. Conclusion: We have combined %%%2%%%-%%%D%%% %%%electrophoresis%%%, Western blotting, and mass spectroscopy to identify some nonimmunoreactive and immunoreactive IROMPs of MH. The proteins may be further utilized to study their role in MH colonization of the nasopharynx.

3/7/6
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0013740825 BIOSIS NO.: 200200334336
Recombinant autofluorescent landmarks for standardization of electrophoretic migration of proteins
AUTHOR: Einhauer Adelheid; Jungbauer Alois (Reprint)
AUTHOR ADDRESS: Institute of Applied Microbiology, University of Agricultural Sciences, Muthgasse 18, A-1190, Vienna, Austria**Austria
JOURNAL: Electrophoresis 23 (7-8): p1146-1152 April, 2002 2002
MEDIUM: print
ISSN: 0173-0835
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Unequivocal identification of unknown protein spot patterns in two-dimensional (%%%2%%%-%%%D%%%) %%%electrophoresis%%% still represents a major problem when performing comparative studies of different %%%2%%%-%%%D%%% %%%electrophoresis%%% gels. Inhomogeneity of gels due to variations in the gel casting procedure, electroendoosmosis and heterogeneity of proteins are major contributions to variations in migration patterns. By fusing green fluorescent protein to a number of well-defined selected proteins (human lysozyme, initiation factor 5a (EIF5a), rapamycin-selective 25 kDa immunophilin (FKBP25), and %%%heat%%% %%%shock%%% %%%protein%%% 90 beta (hsp90)), the isoelectric points and the molecular mass were designed. Proteins were additionally tagged with the FLAG tag enabling rapid purification by immunoaffinity chromatography. The fusion proteins were expressed intracellularly in yeast to avoid heterogeneity caused by post-translational modifications. The quality and applicability was tested in 1-D and %%%2%%%-%%%D%%% %%%electrophoresis%%%. Sharp bands or symmetric spots were obtained. The proteins are considered as a new generation of reference proteins for electrokinetic separation methods.

3/7/7
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0012034418 BIOSIS NO.: 199900294078
Identification of HSP-60 as the specific antigen of IgM produced by BRG-lymphoma cells
AUTHOR: Musante Luca (Reprint); Ulivi Massimo; Cutrona Giovanna; Chiorazzi Nicholas; Roncella Silvio; Candiano Giovanni; Ferrarini Manlio
AUTHOR ADDRESS: Dipartimento di Nefrologia, Istituto Giannina Gaslini, Largo Gerolamo Gaslini, n. 5, 16247, Genova GE, Italy**Italy
JOURNAL: Electrophoresis 20 (4-5): p1092-1097 April-May, 1999 1999
MEDIUM: print
ISSN: 0173-0835
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In previous studies we described a patient with Burkitt's lymphoma and AIDS, whose cells recognized a molecule expressed by normal and malignant breast cells. In the present study, we identified this antigen by two-dimensional (%%%2%%%-%%%D%%%) %%%electrophoresis%%% and Western blotting using the antibody produced by lymphoma cells. The antigen so identified consisted of two clusters of spots with a molecular mass (Mr) of 60 and 50 kDa, respectively. Preparative immobilized pH gradient (IPG) was subsequently used to isolate the clusters of spots of higher molecular masses, from which peptide fragments of approximately 10 aa were separated on reverse-phase chromatography and sequenced. This procedure enabled the identification of the antigen recognized by the lymphoma cells as HSP-60. By means of serological analyses it was possible to identify the lower molecular mass cluster of spots as a molecule related to HSP-60. It is hypothesized that this molecule is a membrane form of HSP-60 that differs fromHSP-60 in a COOH terminal portion.

3/7/8
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0009857525 BIOSIS NO.: 199598325358
Localization of %%%heat%%% %%%shock%%% %%%protein%%% on cell membranes of Phaseolus vulgaris
AUTHOR: Liu Jian; Yang Xiao-He; Wu Xian-Rong
AUTHOR ADDRESS: Beijing Agric. Univ., Beijing 100094, China**China
JOURNAL: Acta Botanica Sinica 37 (2): p87-90 1995 1995
ISSN: 0577-7496
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Chinese

ABSTRACT: Experiment was designed to investigate the expression of %%%heat%%% %%%shock%%% %%%proteins%%% (HSPs) in hypocotyls of Phaseolus vulgaris L. and HSPs localization on cell membranes by means of 35S-Met labelling, fluorography of SDS-PAGE and %%%2%%%-%%%D%%% %%%electrophoresis%%%. The results showed that 70 kD group HSPs were the major labelled proteins and the small HSPs accumulate largely in the fractions of plasma membrane and tonoplast membrane.

3/7/9

DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0008708131 BIOSIS NO.: 199395010397
A possible role of %%%heat%%% %%%shock%%% %%%proteins%%% in human sperm motility
AUTHOR: Yang Rei-Chen (Reprint); Shen Meng-Ru; Chiang Po-Hui; Yang Shu-Ling ; Chen Shun-Sheng
AUTHOR ADDRESS: Dep. of Physiol., Kaohsiung Med. Coll., No. 100, Shih-Chuan 1st Rd., Kaohsiung City 807, Taiwan**Taiwan
JOURNAL: Kaohsiung Journal of Medical Sciences 8 (6): p299-305 1992
ISSN: 0257-5655
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The testicular spermatogenic stem and seminiferous tubular cells selectively synthesize %%%heat%%% %%%shock%%% %%%proteins%%% (Hsps) during heat stress. Hsps, synthesized from testicular cells and leukocytes, are identifical in molecular masses as well as chemical properties. In this study, we induced the Hsps from leukocytes and investigated their in vitro effects on human sperm motility. Semen samples were divided into two parts, washed and unwashed. The whole blood was heated in 43 degree C for 15 minutes for induction of Hsps. A trans-membrane migration method was used to examine the effect of heated blood plasma on human sperm motility. The main heat-induced proteins of leukocytes were detected by %%%2%%%-%%%D%%% %%%electrophoresis%%% and Coomassie blue stain. Leukocytes treated by heat produced a large amount of Hsp72 and Hsp80, while only a small amount was observed in that of nonheated leukocytes. The heated blood plasma inhibited motility of washed sperm in a manner that was dose-dependent. In the presence of seminal plasma fluid, however, the inhibitory effects of heated plasma on human sperm motility could not be observed. It was concluded that the heat-induced substance(s) from leukocytes, which being highly possible the Hsps, interfered the mobility of wash human sperm and the inhibition might be antagonized by seminal plasma.
?
Connection closed by remote host

Connecting via Winsock to Dialog

Logging in to Dialog

Trying 31060000009998...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
****
ENTER PASSWORD:
****
Welcome to DIALOG

Dialog level 05.01.00D

Reconnected in file 5 14apr05 12:07:38
* * *

```
File   5:Biosis Previews(R) 1969-2005/Apr W2
       (c) 2005 BIOSIS

      Set  Items  Description
      ---  -----  -----------
Cost is in DialUnits
? b 410
       14apr05 12:07:38 User217744 Session D911.4
            $0.62    0.107 DialUnits File5
     $0.62  Estimated cost File5
     $0.62  Estimated cost this search
     $0.62  Estimated total session cost   0.107 DialUnits

File 410:Chronolog(R) 1981-2005/Mar
       (c) 2005 The Dialog Corporation

      Set  Items  Description
      ---  -----  -----------
? set hi %%%;set hi %%%
HILIGHT set on as '%%%'%%%
%%%HILIGHT set on as '%%%'
? b5
       14apr05 12:07:42 User217744 Session D911.5
            $0.00    0.100 DialUnits File410
     $0.00  Estimated cost File410
     $0.02  TELNET
     $0.02  Estimated cost this search
     $0.64  Estimated total session cost   0.207 DialUnits

File   5:Biosis Previews(R) 1969-2005/Apr W2
       (c) 2005 BIOSIS

      Set  Items  Description
      ---  -----  -----------
? s heat()shock()protein?
          132844  HEAT
           91472  SHOCK
         1712861  PROTEIN?
      S1   21855  HEAT()SHOCK()PROTEIN?
? s 2()D()gel()electrophoresis
         3182451  2
          729009  D
          230674  GEL
          196277  ELECTROPHORESIS
      S2     443  2()D()GEL()ELECTROPHORESIS
? s s1 and s2
           21855  S1
             443  S2
      S3      24  S1 AND S2
? t s3/7/1-24

 3/7/1
DIALOG(R)File   5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015180932   BIOSIS NO.: 200500087997
```

Localization of the chaperone proteins GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa
AUTHOR: Boilard M; Reyes-Moreno C; Lachance C; Massicotte L; Bailey J L; Sirard M-A; Leclerc P (Reprint)
AUTHOR ADDRESS: 10 Espinay, Quebec City, PQ, G1L 3L5, Canada**Canada
AUTHOR E-MAIL ADDRESS: Pierre.Leclerc@crsfa.ulaval.ca
JOURNAL: Biology of Reproduction 71 (6): p1879-1889 December 2004 2004
MEDIUM: print
ISSN: 0006-3363
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no protein candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane extracts, either an oviductal factor triggered intracellular events resulting in positive effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a positive action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with (35S)-methionine and, upon extensive washes, proteins were separated by two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% to identify the factors suspected to have beneficial effects on spermatozoa. The six major proteins, according to their signal intensity on the autoradiographic film, were extracted from a 2-D gel of oviduct epithelial cell proteins run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to %%%heat%%% %%%shock%%% %%%protein%%% 60 (HSP60) and one to the glucose-regulated protein 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these proteins. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

3/7/2
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015151458 BIOSIS NO.: 200500058523
Proteomic analyses of the response of Arabidopsis chloroplast proteins to high light stress
AUTHOR: Phee Bong-Kwan; Cho Jin-Hwan; Park Sebyul; Jung Jin Hee; Lee Youn-Hyung; Jeon Jong-Seong; Bhoo Seong Hee (Reprint); Hahn Tae-Ryong
AUTHOR ADDRESS: Grad Sch Biotechnol, Kyung Hee Univ, Suwon, 449701, South Korea**South Korea

AUTHOR E-MAIL ADDRESS: shbhoo@khu.ac.kr; trhahn@khu.ac.kr
JOURNAL: Proteomics 4 (11): p3560-3568 November 2004 2004
MEDIUM: print
ISSN: 1615-9853 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 mumol photons m-2.s-1) conditions and then subjected to high light (1000 mumol photons. m-2.s-1) stress. Chloroplasts were then isolated from these plants and both soluble and insoluble proteins were extracted and subjected to two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%%. The resolved proteins were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database analysis. 64 protein spots, which were identified as candidate factors that responded to high light stress, were then selected for analysis and 52 of these were successfully identified using MALDI-TOF-MS analysis. 35 of the 52 identified proteins were found to decrease their expression levels during high light stress and a further 14 of the candidate proteins had upregulated expression levels under these conditions. Most of the proteins that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated proteins were identified as previously well-known high light stress-related proteins, such as %%%heat%%% %%%shock%%% %%%proteins%%% (HSPs), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel proteins that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.

3/7/3
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015131955 BIOSIS NO.: 200500039020
Glycolytic enzymes associated with the cell surface of Streptococcus pneumoniae are antigenic in humans and elicit protective immune responses in the mouse
AUTHOR: Ling E; Feldman G; Portnoi M; Dagan R; Overweg K; Mulholland F; Chalifa-Caspi V; Wells J; Mizrachi-Nebenzahl Y (Reprint)
AUTHOR ADDRESS: Med CtrDept Microbiol and ImmunolPediat Infect Dis Unit, Soroka Univ, IL-84105, Beer Sheva, Israel**Israel
AUTHOR E-MAIL ADDRESS: ymizr@bgumail.bgu.ac.il
JOURNAL: Clinical and Experimental Immunology 138 (2): p290-298 November 2004 2004
MEDIUM: print
ISSN: 0009-9104 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Streptococcus pneumoniae is a leading cause of otitis media, sinusitis, pneumonia, bacteraemia and meningitis worldwide. The drawbacks associated with the limited number of various capsular polysaccharides that can be included in the polysaccharide-based vaccines focuses much attention on pneumococcal proteins as vaccine candidates. We extracted an enriched cell wall fraction from S. pneumoniae WU2. Approximately 150 soluble proteins could be identified by 2D gel electrophoresis. The proteins were screened by 2D-Western blotting using sera that were obtained longitudinally from children attending day-care centres at 18, 30 and 42 months of age and sera from healthy adult volunteers. The proteins were further identified using matrix-assisted laser desorption ionization-time of flight mass spectrometry. Seventeen proteins were antigenic in children and adults, of which 13 showed an increasing antibody response with age in all eight children analysed. Two immunogenic proteins, fructose-bisphosphate aldolase (FBA) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and a control protein with known low immunogenicity, %%%heat%%% %%%shock%%% %%%protein%%% 70 (DnaK), were expressed in Escherichia coli, purified and used to immunize mice. Mouse antibodies elicited to the recombinant (r) FBA and rGAPDH were cross-reactive with several genetically unrelated strains of different serotypes and conferred protection to respiratory challenge with virulent pneumococci. In addition, the FBA used in this study (NP_345117) does not have a human ortholog and warrants further investigation as a candidate for a pneumococcal vaccine. In conclusion, the immunoproteomics based approach utilized in the present study appears to be a suitable tool for identification of novel S. pneumoniae vaccine candidates

3/7/4
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015107361 BIOSIS NO.: 200500014426
Genomic data for alternate production strategies. I. Identification of major contaminating species for cobalt+2 immobilized metal affinity chromatography
AUTHOR: Cai Ying; Moore Misty; Goforth Robyn; Henry Ralph; Beitle Robert (Reprint)
AUTHOR ADDRESS: Dept Chem Engn, Univ Arkansas, 3202 Bell Engn Ctr, Fayetteville, AR, 72701, USA**USA
JOURNAL: Biotechnology and Bioengineering 88 (1): p77-83 October 5, 2004 2004
MEDIUM: print
ISSN: 0006-3592
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Recent advances in technology have allowed for the identification of complex protein mixtures in a rapid fashion. This report highlights the use of 2D gel electrophoresis, mass spectrometry, and database analysis to determine contaminating species of the Escherichia coli genome that are present during immobilized metal affinity chromatography (IMAC), highlighting Co+2 as the affinity ligand. Four proteins

(triosephosphate isomerase, alpha galactosiclase, Hsp90, and glucosamine 6-phosphate synthase) constitute the majority of E. coli proteins that bind and potentially may coelute during chromatography. Results are discussed within the context of changes that when implemented could lead to an increase in IMAC efficiency, not by altering column conditions, but rather by changing the nature of the nuisance proteins that principally reduce column capacity and extend processing times. Such a study illustrates the use of proteome data to aid in bioprocess design. Copyright 2004 Wiley Periodicals, Inc.

3/7/5
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0015049513 BIOSIS NO.: 200400420302
Mechanisms of action of the antidepressants fluoxetine and the substance P antagonist L-000760735 are associated with altered neurofilaments and synaptic remodeling
AUTHOR: Guest Paul C (Reprint); Knowles Michael R; Molon-Noblot Sylvain; Salim Kamran; Smith David; Murray Fraser; Laroque Philippe; Hunt Stephen P; De Felipe Carmen; Rupniak Nadia M; McAllister George
AUTHOR ADDRESS: Neurosci Res Ctr, Merck Sharp and Dohme, Eastwick Rd, Harlow, Essex, CM20 2QR, UK**UK
JOURNAL: Brain Research 1002 (1-2): p1-10 March 26, 2004 2004
MEDIUM: print
ISSN: 0006-8993 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Antidepressants are widely prescribed in the treatment of depression, although the mechanism of how they exert their therapeutic effects is poorly understood. To shed further light on their mode of action, we have attempted to identify a common proteomic signature in guinea pig brains after chronic treatment with two different antidepressants. Both fluoxetine and the substance P receptor (NK1R) antagonist (SPA) L-000760735 altered cortical expression of multiple %%%heat%%% %%%shock%%% %%%protein%%% 60 forms along with neurofilaments and related proteins that are critical determinants of synaptic structure and function. Analysis of NK1R -/- mice showed similar alterations of neurofilaments confirming the specificity of the effects observed with chronic NK1R antagonist treatment. To determine if these changes were associated with structural modification of synapses, we carried out electron microscopic analysis of cerebral cortices from fluoxetine-treated guinea pigs. This showed an increase in the percentage of synapses with split postsynaptic densities (PSDs), a phenomenon that is characteristic of activity-dependent synaptic rearrangement. These findings suggest that cortical alterations of the neurofilament pathway and increased synaptic remodeling are associated with the mechanism of these two antidepressant drug treatments and may contribute to their psychotherapeutic actions. Copyright 2004 Elsevier BY All rights reserved.

3/7/6
DIALOG(R)File 5:Biosis Previews(R)

(c) 2005 BIOSIS. All rts. reserv.

0015026427 BIOSIS NO.: 200400397216
Sinorhizobium meliloti metabolism in the root nodule: A proteomic perspective
AUTHOR: Djordjevic Michael A (Reprint)
AUTHOR ADDRESS: Res Sch Biol SciGenom Interact GrpARC Ctr Excellence Integrat Legume Res, Australian Natl Univ, GPO Box 475, Canberra, ACT, 2601, Australia**Australia
AUTHOR E-MAIL ADDRESS: michael@rsbs.anu.edu.au
JOURNAL: Proteomics 4 (7): p1859-1872 July 2004 2004
MEDIUM: print
ISSN: 1615-9853 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The proteome of the model symbiotic bacterium, Sinorhizobium meliloti was examined to determine the enzymatic reactions and cell processes that occur when S. meliloti occupies the root nodules of Medicago truncatula and Melilotus alba. The proteomes of the nodule bacteria were compared to that of S. meliloti grown under laboratory cultured conditions as an additional control. All the detectable protein spots on the two-dimensional (2-D) gels between pH 4-7 were analyzed. In total, the identity of proteins in 1545 spots from 2-D gels was determined using peptide mass fingerprinting. There were clear differences in the proteome of nodule bacteria and cultured bacteria and putative nodule-specific and nodule suppressed proteins were identified. The data were analyzed using metabolic pathway prediction programs and used to review the biochemical and genetic studies that had been done previously on S. meliloti over several decades. There was a broad congruency between the proteomic and biochemical data when the overall pathways of central carbon and nitrogen metabolism were considered. A selective suite of ABC-type transporters was present in nodule bacteria that were biased towards the transport of amino acids and inorganic ions (P and Fe) suggesting that a highly specialized nutrient exchange was occurring between the nodule bacteria and the host. Proteins prominent in nodule bacteria were those involved in the pathways for vitamin synthesis and stress-related processes (chaperoning, heat shock, detoxification of reactive oxygen species, regulation of stress and osmo-regulation). Some of these proteins were found only in nodule bacteria. These results show the extent of the shift in metabolism that occurs when S. meliloti invades legume plants and establishes a nitrogen fixing symbiosis.

3/7/7
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014897931 BIOSIS NO.: 200400268688
Nuclear matrix protein expressions in hepatocytes of normal and cirrhotic rat livers under normal and regenerating conditions
AUTHOR: Yun Jing-Ping (Reprint); Liew Choong-tsek; Chew Eng Ching; Yin Xiao-Yu; Lai Paul Bo San; Fai Yam Hin; Li H K Richard; Jin Mei-Lin; Ding Ming-Xiao; Li Ming-Tao; Lin Han-Liang; Lau Wan Yee
AUTHOR ADDRESS: Ctr CancDept Pathol, Natl Sun Yat Sen Univ, 651 E Dongfeng Rd, Guangzhou, 510060, China**China

AUTHOR E-MAIL ADDRESS: jpyun@gzsums.edu.cn
JOURNAL: Journal of Cellular Biochemistry 91 (6): p1269-1279 April 15, 2004 2004
MEDIUM: print
ISSN: 0730-2312 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We explored the feasibility of studying nuclear matrix protein (NMP) expressions of the hepatocytes in normal and cirrhotic rat livers with liver regeneration after partial hepatectomy. Sixteen Wistar healthy rats were studied with experimental liver regeneration and/or liver cirrhosis. Two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% was used to generate these NMP compositions from these rat liver samples. Several antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and %%%heat%%% %%%shock%%% %%%protein%%% 70 were used for identification by Western blot. Totally, 41 strongly stained protein Spots were characterized on the 2-D gels. Thirty-four protein spots were detected in all of these rat livers, of which, cytokeratin, vimentin, actin, HNF4alpha, and %%%heat%%% %%%shock%%% %%%protein%%% 70 were identified. B23 was detected in the regenerated livers. Three protein spots (s33, s34, and s35) were detectable only in NMP preparation extracted from the regenerating rat livers after hepatectomy. Another three protein spots (s36, s37, and s38) were detectable only in NMP preparation extracted from thioacetamide-induced cirrhotic rat livers. Under these conditions including experimental liver regeneration and/or liver cirrhosis, Over thirty higher abundance NMPs of hepatocytes were consistently expressed and considered as common and basic NMPs. Some of the NMPs are specific for liver regeneration and may play a critical role in cell proliferation and cell cycle, and some are specific for liver cirrhosis. Copyright 2004 Wiley-Liss, Inc.

3/7/8
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014776735 BIOSIS NO.: 200400157492
F-actin capping (CapZ) and other contractile saphenous vein smooth muscle proteins are altered by hemodynamic stress: A proteomic approach.
AUTHOR: McGregor Emma (Reprint); Kempster Lee; Wait Robin; Gosling Martin; Dunn Michael J; Powell Janet T
AUTHOR ADDRESS: South Wing Laboratory, Proteome Sciences plc, Institute of Psychiatry, 16 De Crespigny Park, London, SE5 8AF, UK**UK
AUTHOR E-MAIL ADDRESS: e.mcgregor@iop.kcl.ac.uk
JOURNAL: Molecular & Cellular Proteomics 3 (2): p115-124 February 2004 2004
MEDIUM: print
ISSN: 1535-9476 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Increased force generation and smooth muscle remodeling follow the implantation of saphenous vein as an arterial bypass graft. Previously, we characterized and mapped 129 proteins in human saphenous

vein medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Here, we focus on actin filament remodeling in response to simulated arterial flow. Human saphenous vein was exposed to simulated venous or arterial flow for 90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%% using a non-linear immobilized pH 3-10 gradient in the first dimension. Proteins were analyzed quantitatively using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 muM) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated protein expression (seven paired vein samples). The %%%heat%%% %%%shock%%% %%%protein%%% HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance (p=0.01), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms (p=0.018). The abundance of actin-capping protein alpha2 subunit CapZ had decreased 3-fold, p=0.04. A 19-kDa proteolytic fragment of actin increased 2-fold, p=0.04. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, p=0.022. The abundance of other proteins associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of proteins involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

3/7/9
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014763705 BIOSIS NO.: 200400131059
Phosphoproteome analysis of cardiomyocytes subjected to beta-adrenergic stimulation: Identification and characterization of a cardiac %%%heat%%% %%%shock%%% %%%protein%%% p20.
AUTHOR: Chu Guoxiang; Egnaczyk Gregory F; Zhao Wen; Jo Su-Hyun; Fan Guo-chang; Maggio John E; Xiao Rui-Ping; Kranias Evangelia G (Reprint)
AUTHOR ADDRESS: Department of Pharmacology and Cell Biophysics, College of Medicine, University of Cincinnati, 231 Albert B. Sabin Way, Cincinnati, OH, 45267-0575, USA**USA
AUTHOR E-MAIL ADDRESS: litsa.kranias@uc.edu
JOURNAL: Circulation Research 94 (2): p184-193 February 6, 2004 2004
MEDIUM: print
ISSN: 0009-7330 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Posttranslational modification of target substrates underlies biological processes through activation/inactivation of signaling cascades. To concurrently identify the phosphoprotein substrates associated with cardiac beta-adrenergic signaling, the mouse myocyte phosphoproteome was analyzed using %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%% in combination with 32P autoradiography. Phosphoprotein spots, detected by silver staining, were identified using

MALDI-TOF mass spectrometry in conjunction with computer-assisted protein spot matching. Stimulation with isoproterenol (1 mumol/L for 5 minutes) was associated with maximal increases in myocyte contractile parameters, and significant stimulation of the phosphorylation of troponin I (190+-23%) and succinyl CoA synthetase (160+-16%), whereas the phosphorylation of pyruvate dehydrogenase (48+-10%), NADH-ubiquinone oxidoreductase (46+-6%), %%%heat%%% %%%shock%%% %%%protein%%% 27 (18+-3%), alphaB-crystallin (20+-3%), and an unidentified 26-kDa protein (29+-7%) was significantly decreased, compared with unstimulated cells (100%). After sustained (30 minutes) stimulation with isoproterenol, only the alterations in the phosphorylation levels of troponin I and NADH-ubiquinone oxidoreductase were maintained and de novo phosphorylation of a phosphoprotein (apprxeq20 kDa and pI 5.5) was observed. The tryptic peptide fragments of this phosphoprotein were sequenced using postsource decay mass spectrometry, and the protein was subsequently cloned and designated as p20, based on its high sequence homology with rat and human skeletal p20. The mouse cardiac p20 contains the conserved domain sequences for %%%heat%%% %%%shock%%% %%%proteins%%%, and the RRAS consensus sequence for cAMP-PKA substrates. LC-MS/MS phosphorylation mapping confirmed phosphorylation of Ser16 in p20 on beta-agonist stimulation. Adenoviral gene transfer of p20 was associated with significant increases in contractility and Ca transient peak in adult rat cardiomyocytes, suggesting an important role of p20 in cardiac function. These findings suggest that cardiomyocytes undergo significant posttranslational modification via phosphorylation in a multitude of proteins to dynamically fine-tune cardiac responses to beta-adrenergic signaling.

3/7/10
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014690671 BIOSIS NO.: 200400061428
Developmentally induced changes of the proteome in the protozoan parasite Leishmania donovani.
AUTHOR: Bente Meike; Harder Simone; Wiesgigl Martina; Heukeshoven Jochen; Gelhaus Christoph; Krause Eberhard; Clos Joachim; Bruchhaus Iris (Reprint)
AUTHOR ADDRESS: Bernhard Nocht Institute for Tropical Medicine, Bernhard Nocht Str. 74, D-20359, Hamburg, Germany**Germany
AUTHOR E-MAIL ADDRESS: bruchhaus@bni.uni-hamburg.de
JOURNAL: Proteomics 3 (9): p1811-1829 September 2003 2003
MEDIUM: print
ISSN: 1615-9853 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In order to proceed through their life cycle, protozoan parasites of the genus Leishmania cycle between sandflies and mammals. This change of environment correlates with the differentiation from the promastigote stage (insect form) to the amastigote stage (intracellular mammalian form). The molecular basis underlying this major transformation is poorly understood so far; however, %%%heat%%% %%%shock%%% %%%protein%%% 90 (HSP90) appears to play a pivotal role. To further elucidate this process we identified proteins expressed preferentially in either of the two life

cycle stages. By using two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% we observed defined changes in the protein pattern. A total of approximately 2000 protein spots were visualized. Of these, 31 proteins were present only in promastigotes. The abundance of 65 proteins increased during heat-induced in vitro amastigote differentiation, while a decreased abundance is observed for four proteins late in amastigote differentiation. Further analyses using matrix-assisted laser desorption/ionization-time of flight mass spectrometry and peptide mass fingerprinting 67 protein spots were identified representing 41 different proteins known from data-bases and eight hypothetical proteins. Further studies showed that most of the stage-specific proteins fall into five groups of functionally related proteins. These functional categories are: (i) stress response (e.g. heat, oxidative stress); (ii) cytoskeleton and cell membrane; (iii) energy metabolism and phosphorylation; (iv) cell cycle and proliferation; and (v) amino acid metabolism. Very similar changes in the 2-D protein pattern were obtained when in vitro amastigote differentiation was induced either by pharmacological inhibition of HSP90 or by a combination of heat stress and acidic pH supporting the critical role for HSP90 in life cycle control.

3/7/11
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014595359 BIOSIS NO.: 200300551790
ANTI - 70 KD %%%HEAT%%% %%%SHOCK%%% %%%PROTEIN%%% AUTOANTIBODIES IN PATIENTS WITH MULTIPLE EVANESCENT WHITE DOT SYNDROME
AUTHOR: Kachi S (Reprint); Nakamura M (Reprint); Nishizawa Y; Uemura A (Reprint); Miyake Y (Reprint)
AUTHOR ADDRESS: Ophthalmology, Nagoya Univ School of Medicine, Nagoya-shi, Japan**Japan
JOURNAL: ARVO Annual Meeting Abstract Search and Program Planner 2003 p Abstract No. 4854 2003 2003
MEDIUM: cd-rom
CONFERENCE/MEETING: Annual Meeting of the Association for Research in Vision and Ophthalmology Fort Lauderdale, FL, USA May 04-08, 2003; 20030504
SPONSOR: Association for Research in Vision and Ophthalmology
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Purpose To report the presence of autoantibodies against the 70 kD %%%heat%%% %%%shock%%% %%%protein%%% in patients with multiple evanescent white dot syndrome (MEWDS). Methods Sera from two patients with MEWDS were subjected to Western blot analysis using bovine retinal proteins. The detected antigen was identified by two-dimensional (%%%2%%% -%%%D%%%) %%%gel%%% %%%electrophoresis%%%, in-gel carboxymethylation and digestion, and mass spectrometry. Results A 70 kD bovine retinal antigen was recognized in the MEWDS sera by Western blot analysis. The protein was identified as a 70 kD %%%heat%%% %%%shock%%% %%%protein%%% by mass spectrometry. The MEWDS sera recognized %%%heat%%% %%%shock%%% %%%protein%%% 70 (Hsp70) and heat shock cognate protein 70 (Hsc70), which are expressed in the retina and are highly homologous with 95% of the amino acid residues identical. Conclusions The sera of the MEWDS patients contain autoantibodies against Hsp70 and Hsc70. This suggests that the

anti-70 kD %%%heat%%% %%%shock%%% %%%protein%%% autoantibody is a strong candidate for the cause of MEWDS. Mass spectrometry is a powerful tool to identify autoantigens in patients with possible autoimmune diseases.

3/7/12
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014260934 BIOSIS NO.: 200300219653
Identification of cellular changes associated with increased production of human growth hormone in a recombinant Chinese hamster ovary cell line.
AUTHOR: Van Dyk Derek D (Reprint); Misztal David R; Wilkins Marc R; Mackintosh James A; Poljak Anne; Varnai Jodie C; Teber Erdahl; Walsh Bradley J; Gray Peter P
AUTHOR ADDRESS: Australian Proteome Analysis Facility, Macquarie University, 2109, Sydney, Australia**Australia
AUTHOR E-MAIL ADDRESS: dvandyk@proteome.org.au
JOURNAL: Proteomics 3 (2): p147-156 February 2003 2003
MEDIUM: print
ISSN: 1615-9853 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A proteomics approach was used to identify the proteins potentially implicated in the cellular response concomitant with elevated production levels of human growth hormone in a recombinant Chinese hamster ovary (CHO) cell line following exposure to 0.5 mM butyrate and 80 muM zinc sulphate in the production media. This involved incorporation of two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and protein identification by a combination of N-terminal sequencing, matrix-assisted laser desorption/ionisation-time of flight mass spectrometry, amino acid analysis and cross species database matching. From these identifications a CHO 2-D reference map and annotated data-base have been established. Metabolic labelling and subsequent autoradiography showed the induction of a number of cellular proteins in response to the media additives butyrate and zinc sulphate. These were identified as GRP75, enolase and thioredoxin. The chaperone proteins GRP78, HSP90, GRP94 and HSP70 were not up-regulated under these conditions.

3/7/13
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0014159644 BIOSIS NO.: 200300118363
Activation of platelet-derived growth factor pathway in human asthmatic pulmonary-derived mesenchymal cells.
AUTHOR: Malmstrom Johan; Tufvesson Ellen; Lofdahl Claes-Goran; Hansson Lennart; Marko-Varga Gyorgy (Reprint); Westergren-Thorsson Gunilla
AUTHOR ADDRESS: Analytical Chemistry, Lund University, 221 00, Lund, Sweden **Sweden
AUTHOR E-MAIL ADDRESS: gyorgy.marko-varga@astrazeneca.com
JOURNAL: Electrophoresis 24 (1): p276-285 January 2003 2003
MEDIUM: print

ISSN: 0173-0835 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cell cultures of mesenchymal type were obtained from biopsies taken after bronchoscopy from patients with asthma. It was possible to achieve outgrowth of fibroblast-like cells from these lung biopsies, which stained for alpha-smooth actin indicating that they were of myofibroblast type. Morphologically, two types of myofibroblasts could be observed: one intermediate form with more stretched cell shape and lamellipodia protrusions, and one more differentiated compact form of myofibroblast. The intermediate form was the most dominant type in these patients, indicating an active ongoing remodelling process. Further studies showed that platelet-derived growth factor (PDGF) might be the factor that stimulates the formation of the intermediate type of myofibroblasts, since it enhance migration of normal human lung fibroblasts 4-fold compared to control through an induced formation of stress fibers and lamellipodia protrusions. Additionally, intracellular signalling pathways involved in migration, such as RhoA and MAPkinase were stimulated 1.5-fold and 3.5-fold, respectively. By using two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and protein identification by peptide mass finger printing matrix assisted laser desporption/ionization - time of flight - mass-spectrometry (MALDI-TOF-MS) it was possible to confirm that PDGF affected the synthesis of proteins involved in the remodelling process, such as collagen VI and posttranslational forms thereof. PDGF also stimulated the production of FK506 binding protein of 65 kDa, a protein involved in smooth muscle differentiaition, and proteins involved in the rearrangement of the cytoskeleton connected to migration such as the actin related protein ARP3, the T-complex protein and the %%%heat%%% %%%shock%%% %%%protein%%% 60. We demonstrate that PDGF has a potential pathological role in asthma and formation of subepithelial fibrosis by inducing changes in the proteome.

3/7/14
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0013689700 BIOSIS NO.: 200200283211
Protein expression during lag phase and growth initiation in Saccharomyces cerevisiae
AUTHOR: Brejning Jeanette (Reprint); Jespersen Lene
AUTHOR ADDRESS: Department of Dairy and Food Science, Food Microbiology, The Royal Veterinary and Agricultural University, Rolighedsvej 30, DK-1958, Frederiksberg C, Denmark**Denmark
JOURNAL: International Journal of Food Microbiology 75 (1-2): p27-38 5 May, 2002 2002
MEDIUM: print
ISSN: 0168-1605
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In order to obtain a better understanding of the biochemical events taking place in Saccharomyces cerevisiae during the lag phase, the

proteins expressed during the first hours after inoculation were investigated by two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and compared to those expressed in late respiratory growth phase. The studies were performed on a haploid strain (S288C) grown in defined minimal medium. Some of the abundant proteins, whose expression relative to total protein expression was induced during the lag phase, were identified by MALDI MS, and the expression of the corresponding genes was assessed by Northern blotting. The rate of protein synthesis was found to increase strongly during the lag phase and the number of spots detected on 2-D gels increased from 502 spots just after inoculation to 1533 spots at the end of the lag phase. During the first 20 min, the number of detectable spots was considerably reduced compared to the number of spots detected from the yeast in respiratory growth just prior to harvest and inoculation (747 spots), indicating an immediate pausing or shutdown in synthesis of many proteins just after inoculation. In this period, the cells got rid of most of their buds. The MALDI MS-identified, lag phase-induced proteins were adenosine kinase (Ado1p), whose cellular role is presently uncertain, cytosolic acetaldehyde dehydrogenase (Ald6p) and (DL)-glycerol-3-phosphatase 1, both involved in carbohydrate metabolism, a ribosomal protein (Asc1p), a fragment of the 70-kDa %%%heat%%% %%%shock%%% %%%protein%%% Ssb1, and translationally controlled tumour protein homologue (Yk1056cp), all involved in translation, and S-adenosylmethionine synthetase 1 involved in biosynthesis reactions. The level of mRNA of the corresponding genes was found to increase strongly after inoculation. By pattern matching using previously published 2-D maps of yeast proteins, several other lag phase-induced proteins were identified. These were also proteins involved in carbohydrate metabolism, translation, and biosynthesis reactions. The identified proteins together with other, yet unidentified, lag phase-induced proteins are expected to be important for yeast growth initiation and could be valuable biological markers for yeast performance. Such markers would be highly beneficial in the control and optimisation of industrial fermentations.

3/7/15
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0013640006 BIOSIS NO.: 200200233517
Multiple-stress resistance in pressure resistant mutants of Escherichia coli
AUTHOR: Aertsen A (Reprint); Hauben K (Reprint); Michiels C (Reprint)
AUTHOR ADDRESS: Katholieke Universiteit Leuven, Heverlee, Belgium**Belgium
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 101 p566 2001 2001
MEDIUM: print
CONFERENCE/MEETING: 101st General Meeting of the American Society for Microbiology Orlando, FL, USA May 20-24, 2001; 20010520
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: High hydrostatic pressure has gained importance as a novel non-thermal preservation technique. However, we have recently reported

the isolation of spontaneous pressure resistant mutants (LMM1010, LMM1020, LMM1030) from a pressure-sensitive E. coli strain, MG1655 (Hauben et al., 1997, Appl. Environ. Microbiol. 63: 945-950). E. coli MG1655 and its pressure resistant mutants were analysed for their resistance to stresses commonly encountered in food environments. Altough these mutants were isolated independently and solely on the basis of pressure resistance, they displayed a remarkable cross-resistance to heat, acid, oxidative and/or osmotic stress. The pattern of enhanced stress resistance differed for each mutant, but none of the mutants was found more sensitive than the parent strain under our challenge conditions. Analysis of the global pattern of protein synthesis by %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%% revealed that mutants LMM1010 and LMM1030, but not LMM1020, produced increased levels of some %%%heat%%% %%%shock%%% %%%proteins%%%, including the chaperones GrpE and DnaK, during exponential growth and at the onset of stationary phase. On the other hand it was demonstrated that heat shock and osmotic shock were able to induce temporary pressure resistance in the wild-type strain. In conclusion we have reason to believe that the acquisition of pressure resistance is linked to improved survival upon exposure to other stress factors, and that pressure resistance could be mediated by the action of chaperones.

3/7/16
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0013557625 BIOSIS NO.: 200200151136
Small %%%heat%%% %%%shock%%% %%%protein%%% p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells
AUTHOR: Willsie Julia K; Clegg James S (Reprint)
AUTHOR ADDRESS: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA **USA
JOURNAL: Journal of Cellular Biochemistry 84 (3): p601-614 2001 2001
MEDIUM: print
ISSN: 0730-2312
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The small heat shock/alpha-crystallin protein p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp Artemia franciscana. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other HSPs in stabilizing nuclear matrix proteins (NMPs), nuclear matrices from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix preparations from control and heat-shocked embryos

showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

3/7/17
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0013118978 BIOSIS NO.: 200100290817
Defining the mycoplasma 'cytoskeleton': The protein composition of the Triton X-100 insoluble fraction of the bacterium Mycoplasma pneumoniae determined by %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%% and mass spectrometry
AUTHOR: Regula J T; Boguth G; Goerg A; Hegermann J; Mayer F; Frank R; Herrmann R (Reprint)
AUTHOR ADDRESS: Zentrum fuer molekulare Biologie Heidelberg (ZMBH) Mikrobiologie, Universitaet Heidelberg, Im Neuenheimer Feld 282, D-69120, Heidelberg, Germany**Germany
JOURNAL: Microbiology (Reading) 147 (4): p1045-1057 April, 2001 2001
MEDIUM: print
ISSN: 1350-0872
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: After treating Mycoplasma pneumoniae cells with the nonionic detergent Triton X-100, an undefined, structured protein complex remains that is called the 'Triton X-100 insoluble fraction' or 'Triton shell'. By analogy with eukaryotic cells and supported by ultrastructural analyses it is supposed that this fraction contains the components of a bacterial cytoskeleton-like structure. In this study, the composition of the Triton X-100 insoluble fraction was defined by electron microscopic screening for possible structural elements, and by two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and MS to identify the proteins present. Silver staining of 2-D gels revealed about 100 protein spots. By staining with colloidal Coomassie blue, about 50 protein spots were visualized, of which 41 were identified by determining the mass and partial sequence of tryptic peptides of individual proteins. The identified proteins belonged to several functional categories, mainly energy metabolism, translation and heat-shock response. In addition, lipoproteins were found and most of the proteins involved in cytadherence that were previously shown to be components of the Triton X-100 insoluble fraction. There were also 11 functionally unassigned proteins. Based on sequence-derived predictions, some of these might be potential candidates for structural components. Quantitatively, the most prevalent proteins were the %%%heat%%%-%%%shock%%% %%%protein%%% DnaK, elongation factor Tu and subunits alpha and beta of the pyruvate dehydrogenase complex (PdhA, PdhB), but definite conclusions regarding the composition of the observed structures can only be drawn after specific proteins are assigned to them, for example by immunocytochemistry.

3/7/18
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0012504939 BIOSIS NO.: 200000223252
Characterization of heat, oxidative, and acid stress responses in Brucella melitensis
AUTHOR: Teixeira-Gomes Ana P (Reprint); Cloeckaert Axel; Zygmunt Michel S
AUTHOR ADDRESS: Laboratoire de Pathologie Infectieuse et Immunologie, Centre de Recherches de Tours, INRA, 37380, Nouzilly, France**France
JOURNAL: Infection and Immunity 68 (5): p2954-2961 May, 2000 2000
MEDIUM: print
ISSN: 0019-9567
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Brucella melitensis is a facultative intracellular pathogen which is able to survive and replicate within phagocytic cells. Therefore, it has to adapt to a range of different hostile environments. In order to understand the mechanisms of intracellular survival employed by virulent B. melitensis 16M, an initial approach consisting of analysis of the differences in patterns of protein synthesis in response to heat, oxidative, and acid pH stresses by two-dimensional (2-D) polyacrylamide gel electrophoresis was used. Depending on the stress, this involved about 6.4 to 12% of the 676 protein spots detected in %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%%. On the basis of N-terminal sequence analysis and database searching, 19 proteins whose level of synthesis was up- or down-regulated by stress conditions were identified. Some of them were previously reported for Brucella, such as BvrR, DnaK, GroEL, and Cu-Zn superoxide dismutase (SOD). Eight other proteins closely matched proteins found in other bacteria: AapJ, alpha-ETF, ClpP, Fe and/or Mn SOD, malate dehydrogenase, IalB, 30S ribosomal protein S1, and pyruvate dehydrogenase E1 component beta subunit. Results indicated that B. melitensis could bring specific regulatory mechanisms into play in response to stress conditions. For example, the ribosome releasing factor in B. melitensis appeared to be a %%%heat%%% %%%shock%%% %%%protein%%%, whereas the ClpP protein, described as a %%%heat%%% %%%shock%%% %%%protein%%% for Escherichia coli, was strongly down-regulated in B. melitensis in response to heat stress. Some of the identified proteins and their potential specific regulation could be required for the adaptation of B. melitensis to environmental stresses encountered in phagocytic cells and possibly for bacterial virulence.

3/7/19
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0010883723 BIOSIS NO.: 199799517783
Hsp70 genes and heat shock factors during preimplantation phase of mouse development
AUTHOR: Christians E (Reprint); Michel E; Renard J-P
AUTHOR ADDRESS: Serv. d'Histol. d'Embryol., Fac. Med. Vet., Univ. Liege ULg, 20 Blvd. de Colonster, B-4000 Liege, Belgium**Belgium
JOURNAL: CMLS Cellular and Molecular Life Sciences 53 (2): p168-178 1997 1997
ISSN: 1420-682X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Heat shock genes are found in all organisms, and synthesis of %%%heat%%% %%%shock%%% %%%proteins%%% is induced by various stressors in nearly all the cells forming these organisms. However, a particular situation is noticed for hsp70 genes in mouse embryos at the beginning of their development. First, spontaneous expression of hsp70 is observed at the onset of zygotic genome activity. Second, inducible expression is delayed until morula or early blastocyst stages. A better understanding of both these points depends on a more careful analysis of hsp70 expression in relation to their major regulators, the heat shock factors. In this review, we will see how the development of the preimplantation embryo highlights the complexity of heat shock gene regulation involving trans-cis interactions and the cellular and nuclear environment.

3/7/20
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0009711980 BIOSIS NO.: 199598179813
The Heat-shock Response and Expression of %%%Heat%%%-%%%shock%%% %%%Proteins%%% in Wheat under Diurnal Heat Stress and Field Conditions
AUTHOR: Nguyen Henry T (Reprint); Joshi Chandrashekhar P; Klueva Natalya; Weng Jian; Hendershot Kerry L; Blum Abraham
AUTHOR ADDRESS: Plant Mol. Genet. Lab., Dep. Plant Soil Sci. Inst. Biotechnol., Texas Tech Univ., Lubbock, TX 79409, USA**USA
JOURNAL: Australian Journal of Plant Physiology 21 (6): p857-867 1994 1994
ISSN: 0310-7841
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The occurrence of %%%heat%%%-%%%shock%%% %%%proteins%%% (HSPs) in response to high temperature stress is a universal phenomenon in higher plants and has been well documented. However, in agriculturally important species, less is known about the expression of HSPs under natural environments. A review of the heat-shock response in wheat (Triticum aestivum L.) is presented and recent results on the expression of wheat HSPs under diurnal stress and field conditions are reported. In the field experiment, flag leaf blade temperatures were obtained and leaf blades collected for northern blot analysis using HSP 16.9 cDNA as a probe. Temperatures of leaf blades ranged from 32 to 35 degree C under the tested field conditions at New Deal near Lubbock, Texas. Messenger RNAs encoding a major class of low molecular weight HSPs, HSP 16.9, were detected in all wheat genotypes examined. The results suggested that HSPs are synthesized in response to heat stress under agricultural production, and furthermore, that HSPs are produced in wheats differing in geographic background. In the controlled growth chamber experiment. HSP expression in two wheat cultivars, Mustang (heat tolerant) and Sturdy (heat susceptible) were analysed to determine if wheat genotypes differing in heat tolerance differ in in vitro HSP synthesis (translatable HSP mRNAs) under a chronic, diurnal heat-stress regime. Leaf tissues were collected from seedlings over a time-course and poly (A)+ RNAs were isolated for in vitro translation and %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%%. The protein profiles shown in the 2-D gel analysis revealed that there were not only quantitative differences of individual HSPs between these

two wheat lines, but also some unique HSPs which were only found in the heat tolerant line. This data provides evidence of a correlation between HSP synthesis and heat tolerance in wheat under a simulated field environment and suggests that further genetic analysis of HSPs in a segregating population is worthy of investigation. In conclusion, the results of this study provide an impetus for the investigation of the roles of HSP genes in heat tolerance in wheat.

3/7/21
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0009165554 BIOSIS NO.: 199497186839
Induction of a heat shock response (HSP 72) in rat embryos exposed to selected chemical teratogens
AUTHOR: Mirkes Philip E (Reprint); Doggett Barbar; Cornel Leanne
AUTHOR ADDRESS: Dep. Pediatr. RD-20, Univ. Washington, Seattle, WA 98195, USA**USA
JOURNAL: Teratology 49 (2): p135-142 1994 1994
ISSN: 0040-3709
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A monoclonal antibody to the 72 kD %%%heat%%% %%%shock%%% %%%protein%%% (HSP 72), Western blot analysis and %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%%/autoradiography were used to determine whether selected chemical teratogens induced the synthesis and accumulation of HSP 72 in postimplantation rat embryos exposed in vitro. The chemical teratogens studied include N-Acetoxy-2-acetylaminofluorene (N-Ac-AAF), cadmium chloride (CAD), cyclophosphamide (CP), sodium arsenite (AS), and sodium salicylate (SAL). Exposures to test chemicals were selected that produced obvious embryotoxicity characterized by abnormal development and growth retardation. Of the five chemical teratogens studied, AS and SAL induced the synthesis and accumulation of HSP 72 in day 10 rat embryos. The kinetics of HSP 72 accumulation, however, differed between AS- and SAL-treated embryos. Maximal levels of HSP 72 were observed 24 hours after AS exposure and 10 hours after SAL exposure. N-Ac-AAF, CD, and CP induced obvious embryotoxicity; however, none of these chemical teratogens induced HSP 72 at any of the timepoints assayed. Although only a small sample of chemical teratogens was studied, our results suggest that the heat shock response, characterized by the synthesis and accumulation of HSP 72, is not a general biomarker for chemical teratogens.

3/7/22
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0008195341 BIOSIS NO.: 199293038232
COMPARISON OF THE NUCLEAR AND CYTOSOLIC FORMS OF THE AH RECEPTOR FROM HEPA 1C1C7 CELLS CHARGE HETEROGENEITY AND ATP BINDING PROPERTIES
AUTHOR: PERDEW G H (Reprint)
AUTHOR ADDRESS: DEP FOODS NUTRITION, PURDUE UNIVERSITY, WEST LAFAYETTE, INDIANA 47907, USA**USA

JOURNAL: Archives of Biochemistry and Biophysics 291 (2): p284-290 1991
ISSN: 0003-9861
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: 2-[-1-2-5I]Iodo-7,8-dibromo-p-dioxin ([125I]Br2DpD) and 2-[125I]Iodo-3-azido-7,8-dibromo-p-dioxin ([125I]N3Br2-DpD)are both capable of binding to the Ah receptor (AhR) with a high degree of specificiy in cultured Hepa 1c1c7 cells. After incubation with either [125i]N3Br3DpD or [125I]Br2DpD Hepa 1c1c7 cytosolic and high salt nuclear extracts were analyzed by sucrose density gradient analysis with the following results: (i) With both radioligands an .apprx. 9 S form of the AhR was observed in cytosolic extracts. (ii) Nuclear extracts labeled with [125I]N3Br2DpD revealed both .apprx. 6 S and .apprx. 9 S forms of the AhR. (iii). In contrast, analysis of nuclear extracts labeled with [125I]Br2DpD revealed only an .apprx. 6 S form of the AhR. The .apprx. 9 S [125I]N3Br2DpD-labeled AhR was preferentially extracted with 100 mM KCl from a nuclear fraction and mixed with monoclonal antibody 8D3, an anti-90-kDa %%%heat%%% %%%shock%%% %%%protein%%% antibody. Monclonal antibody 8D3 was able to bind to the .apprx. 9 S nuclear form of the AhR and caused the receptor to sediment as a heavier complex on sucrose density gradients. This would indicate that the AhR can reside in the nucleus bound to 90-kDa %%%heat%%% %%%shock%%% %%%protein%%%. The [125I]N3Br2DpD-labeled .apprx. 6 peak fractions were collected and subjected to denaturing two-dimensional gel electrophoresis. A comparison of [125I]N3Br2DpD-labeled cytosolic (9 S) AhR preparations with the nuclear (6 S) AhR by %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%% was performed. The cytosolic form of the AhR was present in an apparent pI range of 5.2-5.7; the nuclear form focused between 5.5 and 6.2. The [125I]N3Br2DpD-labeled nuclear extracts were incubated with ATP-agarose and 43% of the photoaffinity-labeled AhR bound to the affinity gel. In contrast, .apprx. threefold lower binding of [125I]N3Br2DpD-labeled receptor was obtained when GTP-, AMP-, or ADP-agarose was used. Only 2% of the [125I]N3Br2DpD-labeled cytosolic AhR was able to bind to ATP-agarose. These results suggest that after the AhR translocates into the nucleus the following biochemical changes occur: (i) The sedimentation value for the AhR changes from an .apprx. 9 S to an .apprx. 6 species. (ii) The AhR attains the ability to bind with specificity to ATP. (iii) The AhR undergoes a shift to a more basic pI.

3/7/23
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0007709225 BIOSIS NO.: 199191092116
COMPREHENSIVE TWO-DIMENSIONAL GEL PROTEIN DATABASES OFFER A GLOBAL APPROACH TO THE ANALYSIS OF HUMAN CELLS THE TRANSFORMED AMNION CELLS AMA MASTER DATABASE AND ITS LINK TO GENOME DNA SEQUENCE DATA
AUTHOR: CELIS J E (Reprint); GESSER B; RASMUSSEN H H; MADSEN P; LEFFERS H; DEJGAARD K; HONORE B; OLSEN E; RATZ G; ET AL
AUTHOR ADDRESS: INST MED BIOCHEM AND BIOREGULATION RES CENTRE, OLE WORMS ALLE, BUILD 170, UNIVERSITY PARK, DK-8000 AARHUS C, DENMARK**DENMARK
JOURNAL: Electrophoresis 11 (12): p989-1071 1990
ISSN: 0173-0835
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A total of 3430 polypeptides (2592 cellular; 838 secreted) from transformed human amnion cells (AMA) labeled with [35S]methionine were separated and recorded using computer-aided two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%%. A master 2-D gel database of cellular protein information that includes both qualitative and quantitative annotations has been established. The protein numbers in this database differ from those reported in an earlier version (Celis et al. Leukemia 1988,2,561-602) as a result of changes in the scanning hardware. The reported information includes: percentage of total radioactivity recovered from the gels (based on quantitations of polypeptides labeled with a mixture of 16 14C-amino acids), protein name (including credit to investigators that aided identification, antibody against protein, cellular localization, (nuclear, 40S hnRNP, 20S snRNP U5, proteasomes, endoplasmic reticulum, mitochondria, Golgi, ribosomes, intermediate filaments, microfilaments and microtubules), levels in fetal human tissues, partial protein sequences (containing information on 48 human proteins microsequence so far), cell cycle-regulated proteins, proteins sensitive to interferons .alpha., .beta., and .gamma., %%%heat%%% %%%shock%%% %%%proteins%%%, annexins and phosphorylated proteins. The results presented should be considered as the initial phase of a joint effort between our laboratories to undertake a general and systematic analysis of human proteins. Using this integrated approach it will be possible to identify phenotype-specific proteins, to microsequence them and store the information in the database, to identify the corresponding genes, to search for homology with previously characterized proteins and to study the function of groups of proteins (pathways, organelles, etc.) that exhibit interesting regulatory properties. In particular, the 2-D gel protein database may become increasingly important in view of the concerted effort to map and sequence the entire human genome.

3/7/24
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0007663276 BIOSIS NO.: 199191046167
%%%HEAT%%%-%%%SHOCK%%% %%%PROTEIN%%% SYNTHESIS AND ACCUMULATION IN DIPLOID WHEAT
AUTHOR: VIERLING R A (Reprint); NGUYEN H T
AUTHOR ADDRESS: DEP AGRONOMY, HORTICULTURE ENTOMOL, TEXAS TECH UNIV, LUBBOCK, TEXAS 79409, USA**USA
JOURNAL: Crop Science 30 (6): p1337-1342 1990
ISSN: 0011-183X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Plants synthesize a set of proteins, called %%%heat%%%-%%%shock%%% %%%proteins%%% (HSPs) under high-temperature stress. These proteins may play a role in the genetic control of thermal tolerance in plants. The objective of this study was to determine if genotype differences exist in the synthesis and accumulation of HSPs in diploid wheat Triticum monococcum L. Plants of three T. monococcum accessions

were heat shocked at 37.degree.C in a controlled condition for 1 h and HSPs were labeled in vivo with 35S-methionine for 3 h. Analysis of HSPs separated by two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% showed qualitative and quantitative diversity of HSP synthesis in T. monococcum. In order to study HSP accumulation, plants were heat shocked at 37.degree.C for 8 h and 2-D separated HSPs were visualized by silver staining. Both qualitative and quantitative diversity of HSP accumulation was observed. Optical density (visible light) of 34 HSPs ranged from 0.33 to 44.64 on silver-stained gels and from 0.21 to 37.64 on labeled gels. %%%Heat%%%-%%%shock%%% %%%proteins%%% unique to individual accessions were identified. The identification of genetic variability in HSP synthesis within diploid wheat provides a useful tool for genetic and physiological studies of the role of HSPs in higher plants.

```
? ds

Set     Items   Description
S1      21855   HEAT()SHOCK()PROTEIN?
S2        443   2()D()GEL()ELECTROPHORESIS
S3         24   S1 AND S2
? s s3 and stabil?
              24  S3
          217939  STABIL?
      S4       1  S3 AND STABIL?
? t s4/7/1

 4/7/1
DIALOG(R)File   5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.
```

0013557625 BIOSIS NO.: 200200151136

Small %%%heat%%% %%%shock%%% %%%protein%%% p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells

AUTHOR: Willsie Julia K; Clegg James S (Reprint)
AUTHOR ADDRESS: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA **USA

JOURNAL: Journal of Cellular Biochemistry 84 (3): p601-614 2001 2001
MEDIUM: print
ISSN: 0730-2312
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The small heat shock/alpha-crystallin protein p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp Artemia franciscana. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other HSPs in %%%stabilizing%%% nuclear matrix proteins (NMPs), nuclear matrices from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional (%%%2%%%-%%%D%%%) %%%gel%%% %%%electrophoresis%%% and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the

case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix preparations from control and heat-shocked embryos showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

```
? log y
      14apr05 12:11:41 User217744 Session D911.6
           $8.37    1.455 DialUnits File5
             $50.00  25 Type(s) in Format  7
          $50.00  25 Types
    $58.37  Estimated cost File5
     $1.06  TELNET
    $59.43  Estimated cost this search
    $60.07  Estimated total session cost   1.662 DialUnits
Logoff: level 05.01.00 D  12:11:41
```